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(54) Title: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

(57) Abstract: The invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin and a method for identification of the specific animal from a given biological sample.

UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

TECHNICAL FIELD

The invention relates to the identification of novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin at species and sub-species sources. The invention also provides a method for the identification of fragments on mitochondrial cytochrome b gene in biological material of unknown origin.

BACKGROUND ART

A large number of studies in evolutionary biology utilize phylogenetic information obtained from mitochondrial cytochrome b gene. It has been identified a potent molecule to distinguish the phylogenetic depth of different lineages to family, genus and species in molecular taxonomy¹⁻⁶⁶. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in public databases such as GenBank, NCBI (<http://www.ncbi.nlm.nih.gov>) etc. We have utilized this capacity of cytochrome b gene in establishing the identity of the origin of animal parts and product to its family, genus and species sources. The technique developed is based on a pair of universal primer that can amplify a small fragment of cytochrome b gene from a vast range of animal species.

Establishing identity of confiscated animal parts and products is a great challenge to law enforcement agencies because none of the methods available till date is too efficient to reveal the identity of animal remains beyond a reasonable doubt. Morphological markers, described for certain species allow the identification of complete specimen of animals⁶⁷. However, a complete specimen is confiscated very rarely by the investigation agencies; therefore, these marker are not practical in wildlife forensics. The biochemical traits such as the bile characteristics⁶⁸ blood haem analysis^{69,70} etc. have also been employed in wildlife forensic for identification of individual species. The difficulty of these markers are that these markers are limited in number and are rarely found in their natural forms in which these were originally described as the characteristic of a particular species.

The molecular approaches such as micro-satellite based identification⁷¹, Restriction fragment length polymorphism analysis of mitochondrial genes or PCR based species specific STS markers require the prior information of the species to establish the identity^{72,73}. These methods also need a significant amount of DNA material to be analysed. We may not have the prior information about the species origin of confiscated animal parts and product in forensics, therefore, these methods are not really useful and

practical in wildlife identification. The technique invented by us is universal, therefore does not require any background information to establish the identity of any unknown confiscated remains at family, genus and species sources. Being a PCR based procedure it can be applied with trace amount of any biological material. Because the amplicon length 5 is small (472 bp); therefore, it can work perfectly with the mutilated remains, which are commonly seized by the crime investigation agencies. It does not require the large amount of genetic material i.e. DNA to be analyzed to establish the identity, hence, can detect a minute amount of adulteration in food products. The procedure described is simple and very fast. Due to the said advantages, the procedure invented by us is most suited for 10 forensic wildlife identification.

OBJECTS OF THE INVENTION

The main object of the invention is to identify a fragment on mitochondrial cytochrome b gene capable of significantly discriminating among various evolutionary lineages of 15 different animal species.

Another object is to identify a fragment on mitochondrial cytochrome b gene which is flanked by the highly conserved sequences at a vast range of animal species.

Yet another object is to detect a fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.

20 Still another object is to develop the universal primers to amplify the fragment on mitochondrial cytochrome b gene using polymerase chain reaction.

Another object is to develop a PCR protocol that works universally with DNA template of any unknown origin (i.e. all the animal species).

25 Yet another object is to provide a universal method for identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

Still another object is to provide a universal method of animal identification to establish the crime with the criminal beyond a reasonably doubt.

30 Another object is provide a universal method to establish the identity of biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

35 Yet another object is to provide a universal method for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation to the wildlife resources could be controlled.

Still another object is to provide a universal technique to have an idea of the geographical location of the commitment of wildlife crime based on the haplotype of poached animal identified by the universal primer invented.

Another object is to provide a universal technique of animal identification to detect the 5 adulteration of animal meat/products in vegetarian food product for the purpose of food fortification, by the food fortification agencies.

Yet another object is to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as 10 if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.

Another object is to invent and authenticate a universal technique that can be converted to a (a) 'MOLECUALR KIT' and (b) 'DNA CHIPS' based application to meet the requirements of above objectives.

15 SUMMARY OF THE INVENTION

Accordingly, the invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin

DETAILED DESCRIPTION OF THE INVENTION

20 Keeping in view the above objectives, the cytochrome b gene sequences (1140 bp) of 221 distantly related animal species (listed in Table 1) representing various families were obtained from public database NCBI (<http://www.ncbi.nlm.nih.gov>). These sequences were aligned using the software *Clustal X(1.8)*(NCBI, USA) and a fragment (of 472 bp, alignment shown in Table 2) of gene was identified which had all the features mentioned 25 above under column 1, 2 and 3 of sub-heading 'Objectives of invention'. As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (*)) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to 30 their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antilope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:
Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*:

"taccatgaggacaaatatctttttagggacaacagtcatcaccaatcccttcagcaatcccatacatcggtacaaaccttaga
atgaatctgaggagggtctcagtagataaagcaacccttacccgattttgccttccactttatctcccatattatcattgcagccctt
accatagtacacccatgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaaattccattccac
ccctactacactatcaaagatattcttaggagctactatttaaccctatgctctagtcctattctcaccggaccttgtggag
5 acccagacaactatacaccagcaaacccacttaatacacccccacatatcaagccgaatgatacttcatttgcatacgcaatcc
ccgatcaattcctaacaaacttaggagg".

A pair of universal primer was designed to amplify this fragment in polymerase chain reaction (PCR). These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of *Antelope cervicapra*, a representative animal species for this invention.

10 We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India. These primers work universally because its 3' end are highly conserved amongst a vast range of animal

15 species (shown in Table 2). As mentioned above, the DNA fragment (sequence of which is shown above) targeted by these primers is highly polymorphic inter-specifically; however, it is monomorphic among the individual of same species (Tables 6, 7a, 7b, 7c, 7d and 8, respectively). These unique features of the targeted region enable these primers to generate the molecular signatures of an individual species; thereby, enabling them to differentiate

20 amongst the animals of different species (see in Figure 1c). The variation within the fragment amplified by these primers increase with increasing distances of evolutionary lineages of two animals (Table 8). These unique features of the fragment amplified by the universal primers 'mcb398' and 'mcb869' invented by the applicants fulfill the objectives of invention.

25 Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using

'BLAST software'⁷³, it indicates identity of the family, genus or species of the analyzed 30 material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. The complete procedure involved in the analyses (the word, 'analyses' should be understood with the stepwise procedure to establish the identity of the biological remain of any unknown animal origin for the aims mentioned in columns

1-13 under sub-heading ‘Objectives of invention’) is briefed under ‘Examples 5 and 6, respectively, as well as illustrated in Figures 1a, 1b and 1c, respectively.

BRIEF DESCRIPTION OF DRAWING AND TABLES

Figure 1a. Illustration of the step-wise procedure involved in *analyses*. The unknown biological material i.e. ‘adil.flesh’ refers to the confiscated skin mentioned in ‘Example 6’. The arrow marks indicate the stepwise procedure involved. The brief description of Figure 1a is as follows:

The biological material i.e. the confiscated skin ‘adil.flesh’ was subjected to DNA isolation using the standard procedures⁷⁴. The DNA obtained was amplified using the primers ‘mcb398’ and ‘mcb869’ in PCR, fractionated in 2% (w/v) agarose gel, visualized and photographed under UV light using Gel Documentation System (Syngene, USA). The lane ‘M’ shown in the photograph represents the molecular weight marker (Marker XIII, Boehringer mannheim). Lane 1 shows the PCR amplicon (472 bp) obtained from ‘adil.flesh’ using primers ‘mcb398’ and ‘mcb869’. The PCR amplicon obtained were sequenced at both the strand using “ABI Prism 3700 DNA Analyzes, PE-Applied Bio-systems). The chromatogram shows the sequences (about 80 bp long, i.e. between 150-230 bp of sequence (328 bp), revealed from the PCR product of 472 bp length) obtained from ‘adil.flesh’.

Figure 1b. Illustrates the further steps involved in *analyses*. The sequence (328 bp) revealed from ‘adil.flesh’ was subjected to homology search in *nr* (i.e. non-redundant) database of National Centre for Biological Information (NCBI), USA. The sequences producing significant alignments are shown along with its bits score and E values. It indicates the extent of homology amongst the sequence enquired (i.e. the 328 bp sequence from adil.flesh) and the sequences registered in *nr* database of NCBI. BLAST analysis revealed the highest homology of the sequence revealed from ‘adil.flesh’ with the sequence of *Panthera pardus* (gene bank registration number ‘AY005809’), indicating the identity of adil.flesh as that of a leopard (*Panthera pardus*) origin. Figure 1b further illustrates the multiple alignments of the sequences obtained from reference animals (listed in Table 5) along with the sequence obtained from ‘adil.flesh’. The sequences of ‘adil.flesh’ is similar to the sequences of ‘gz1L’ further confirming the identity of the source of confiscated remain ‘adil.flesh’ as that of a *Panthera pardus* origin.

Figure 1c illustrates the NJ-tree (Neighbor Joining tree) constructed using CLUSTAL X (1.8) from the sequences revealed from ‘adil.flesh’ and reference animals listed in Table 5.

The animals belonging to similar species cluster together; however, the animals of different species group in different clusters. The confiscated material under investigation (i.e. 'adil.flesh') clusters with 'gz1L' (i.e. the known normal leopard '*Panthera pardus*') indicating the identity of the species of 'adil.flesh' as that of a *Panthera pardus* source.

5 **Figure 2** shows the Agarose gel electrophorogram showing the PCR amplicons (472 bp) obtained from the reference animals of family felidae listed in Table 5, using universal primers 'mcb398 and 'mcb869'. Description of different lanes is as follows:

Lanes 1-21: The PCR profiles of the animals 1-21, respectively, listed in Table 5.

Lane 22: The PCR profiles of DNA isolated from confiscated skin of unknown animal
10 origin 'i.e. adil.flesh'

Lane 23: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

Figure 3. Shows PCR amplicons obtained from animals listed in Table 9. The primers used in PCR are 'AFF' and 'AFR'. The description of different lanes shown is as follows:

15 Lane 1-4: The PCR profiles of animals 1-4, respectively, listed in Table 9, showing amplicons of 354 bp.

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

Figure 4. Shows PCR amplicons obtained from animals listed in Table 12. This experiment demonstrates the universal nature of our primers among a vast range of animal
20 species. Description of different lanes shown is as follows:

Lanes 1-23: The PCR profiles of the animals 1-23, respectively, listed in Table 12. The PCR product of 472 bp is amplified universally from all the animal species analyzed.

Lane 24: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

25 **Table 1.** List of 221 animal species used for *In-silico* analysis to design the universal primers 'mcb398' and 'mcb869'. Table also demonstrate the 'P,S scores' of 'mcb398' and 'mcb869' for different templates. The descriptions of various symbols used in this table are as follows:

Symbol (#) refers to Number

30 Symbol (*) refers to the animal species which is either protected species (listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972), or an endangered/rare animal species

Symbol ([§]P,S/F) refers to Probability of match and Stability of match of primer 'mcb398' with different templates (i.e. the cytochrome b gene from different species origin). A higher P, S score refers to the higher probabilities of significant amplification of specific

template by the primer. It is calculated by *Amplify (1.2)* software.

Symbol (^P,S/R) refers to Probability of match and Stability of match of primer 'mcb869' with different templates. A higher P,S score refers to the higher probabilities of significant amplification of specific template by the primer. It is calculated by *Amplify (1.2)* software.

5 **Table 2.** Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene (identified by inventors to fulfill the requirements of column 1, 2 and 3 mention under sub-heading 'Objectives of invention') of 221 animal species listed in Table 1. Alignments also show the binding sites for universal primers 'mcb398' and 'mcb869'. The symbol (*) refers to the nucleotide bases which are conserved amongst 221 animal species 10 listed in Table 1). The alignments have been done using software *CLUSTAL X (1.8)*. The nucleotide positions that are unmarked are variable amongst 221 animal species analyzed. These variable sites together constitute the molecular signature of an individual species, giving rise to molecular basis of species identification by our primers.

15 **Table 3.** Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'mito' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *felis catus* cytochrome b gene sequence (genbank registration number NC_001700.1, bits score 365, E value, e-101) registered in NCBI database (bits score 365 and E value e-101). It gives an indication that the species of analyzed material belongs to family felidae. It also fulfills the requirements 20 of column 6 mention above under sub-heading 'Objectives of invention'.

25 **Table 4.** Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'nr' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *Panthera pardus* cytochrome b gene sequence (genbank registration number AY005809, bits score 603, E value, e-170) registered in NCBI database. It gives an indication that the species of analyzed material belongs to *Panthera pardus* origin. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

30 **Table 5.** Reference animal belonging to family felidae selected for comparison with 'adil.flesh' to confirm the findings of BLAST analysis results of which are mentioned in Table 3 and 4, respectively. The animals listed in SN. 1-21 represent different species of family felidae. SN. 22 and 23 are primate species taken for out-group comparisons.

Table 6 Multiple sequence alignments of cytochrome b sequences (328 bp) revealed from 'adil.flesh' and reference animals listed in Table 5. The positions that have a common nucleotide in all the animal species under investigation are shown with a star (*) mark;

however, the positions that are variable in any of the animals under investigation are unmarked. The nucleotides at these positions constitute the molecular signature of an individual species, which are unique and highly specific for its species. These signatures are the molecular basis of identification of individual animal species using our primers
5 'mcb398' and 'mcb869'.

Table 7 (Tables 7a, 7b, 7c and 7d). The comparison of the molecular signatures of different animal species investigated along with 'adil.flesh', the confiscated skin of unknown animal origin. This table demonstrates the variable positions (i.e. the positions which are not marked with star (*) symbol in Table 6), amongst the 328 bp fragment
10 revealed from the animals listed in Table 5. The dot (.) mark represents the presence of the similar nucleotide as listed in lane 1 i.e. the sequence from "adil.flesh" at that position. It demonstrates that the signatures of each species are unique and specific to its species. The molecular signatures of 'adil.flesh' are comparable (except for position 37 which has a transition from 'T' to 'C') to the molecular signature of 'gz1L' i.e. the known leopard
15 'Panthera pardus' source, indicating the identity of the source of confiscated skin 'adil.flesh' as that of a leopard 'Panthera pardus' source. The nucleotide variations (at the positions 153, 198, 223, 264, among the known leopards, (i.e. gz1L, gz2L, and gz3L, respectively)), give an idea about the geographical habitat of each animals. Various studies referring to molecular evolution of different animal species support this hypothesis⁷⁵;
20 however, it could further be confirmed by taking the reference animals from different geographical areas and analyzing by our primers 'mcb 398' and 'mcb869'. If we could generate the database of different haplotypes (i.e. habitat specific molecular signatures) of the animal species, it would also enable our primers to reveal the geographical location of the commitment of wildlife crime.

25 **Table 8.** Percent similarity matrix calculated by pair-vise comparisons of nucleotide sequences aligned (illustrated in Table 6). The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity (99.7% and 98.2%, with the lineages of animals 'gz2L' and 'gz3L', respectively) with the sequences obtained from known normal leopard source, indicating its identity as that of a leopard origin. The
30 similarity matrix has been calculated using the software *PHYLIP* (3.5).

Table 9. Animals selected for validation of minimum P,S score for efficient amplification of cytochrome b gene of different origin by the primers 'mcb398' and 'mcb869'. P,S score of primers 'AFF' and 'AFR' for these animals are shown.

Table 10. BLAST analysis of primers 'mcb398' in *nr* database of NCBI . It demonstrates

that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer

Table 11. BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates

5 that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

Table 12. Other animal belonging to distantly related animal species, investigated to

10 confirm the universal nature of primers 'mcb398' and 'mcb869'. Gel photograph showing the PCR amplicons from these animals are shown in Figure 4.

The mitochondrial cytochrome b gene has very widely been used in molecular taxonomic studies. It has immense capabilities to reveal different evolutionary lineages of animals in family, genus and species specific manner. It has also been used to classify the population

15 of a particular species according to its demographic distributions⁷⁵. The vast database of cytochrome b sequences of different animal species has accumulated in public databases such as Genbank and NCBI¹⁻⁶⁵. We have explored these unique characteristics of

cytochrome b gene to establish the identity of confiscated remains of any unknown animal by inventing a pair of novel primers, 'mcb398' and 'mcb869', that can amplify a small

20 fragment (472 bp) of cytochrome b gene of wide range of animal species in universal manner. These primers work universally because its 3' ends target within a highly conserved region.

The fragment of cytochrome b gene identified had all the features mentioned in columns 1,

2 and 3 listed under sub-heading 'Objective of invention'. We identified this fragment by

25 aligning the cytochrome b gene sequences (1140 bp) of 221 different animal species listed in Table 1. These sequences are publicly available in NCBI DNA databases. These

sequences were aligned using the software *CLUSTAL X* (1.8). As mentioned before, the

472 bp fragment of cytochrome b gene identified by us to have the features mentioned in

columns 1, 2 and 3 listed under sub-heading 'Objective of invention' includes the

30 nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to

870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (*)) in Table

2, the nucleotide sequences of this fragment are highly variable amongst the animal

species, revealing the identity of the biological material belonging to that of an unknown

animal origin by the procedure invented by us. As for identity of this fragment we are

considering *Antilope cervicapra* as a representative species, and the sequence the above fragment of cytochrome b gene of *Antilope cervicapra* is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

"taccatgaggacaaatatctttgaggagaacagtcatcaccaatccttcagcaatcccatacatcggtacaaaccttaga
 5 atgaatctgaggagggtctcagtagataaagcaacccttacccgattttcgccctccactttatcctccatttatgcagccctt
 accatagtacacctactgttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaaaatccatccac
 ccctactacactatcaaagatatcttaggagctctactattaatttaaccctcatgctctagtcctatttcacccgacctgctggag
 acccagacaactatacaccagcaaacccacttaatacacccccacatatcaagccgaatgatactcctattgcatacgcaatcct
 ccgatcaattcctaacaaacttaggagg

- 10 Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species. Each species in table 2 has been represented by a unique code, which is decoded in Table 1. We selected these species to represent the vast range of animal families of distant orders. Of 221 species, about 65 were the protected/endangered or rare species listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972). These species are marked 15 with symbol (*) in Table 1. The NCBI accession number refers to its registration number in NCBI database and the number in superscript represent the reference cited. Based on the aligned cytochrome b sequences of different 221 animal species the primers designed were as follow:

Primers name	Sequence (5'-3')
--------------	------------------

20 'mcb398' "TACCATGAGGACAAATATCATTCTG"

'mcb869' "CCTCCTAGTTGTTAGGGATTGATCG"

Tables 2, 10 and 11, respectively, demonstrates that the 3' ends of the primers are highly

conserved amongst all the animal species analyzed *in-silico* (In total 221 animal species listed in Table 1 and about 500 species listed in Tables 10 and 11, respectively) Also, the

25 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e.

the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different

software viz., 'Amplify (1.2)', 'Primer3' (<http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>) as well as manually. . We assigned the P,S score (P=Probability of

match, S=Stability of match) to the primers for each template using the software *Amplify* (1.2).

The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for

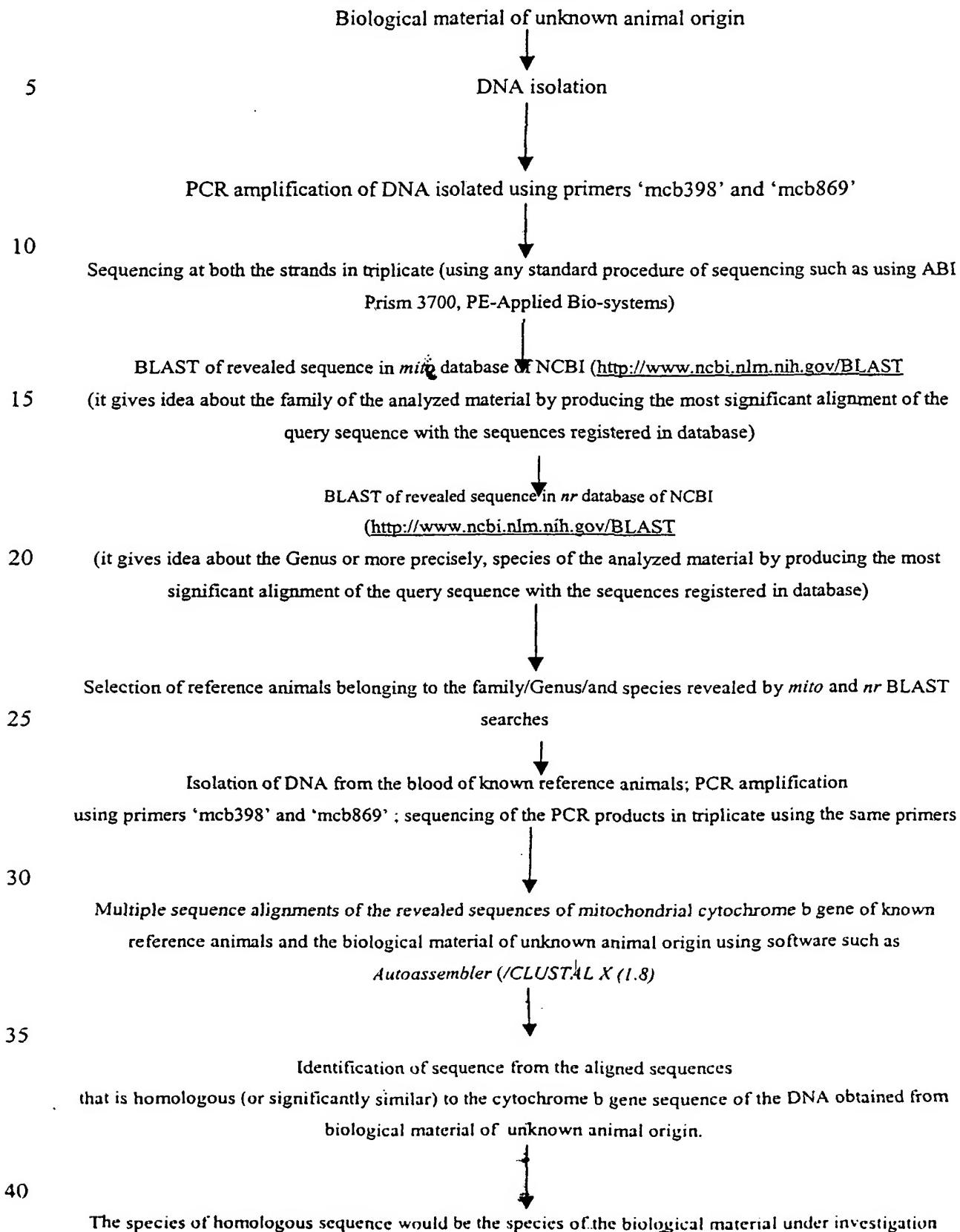
30 'mcb398' was 98.63 (i.e. the situation where the primer has perfect match with template);

however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were 5 *Eumeces egredios* and *Equus ainus*. *Eumeces egredios* had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus ainus* was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S 10 score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= 5'tagtagaaatgaatctgaggagg3' and AFR=5'atgcaaataatggaaatgtatcattc3') having more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability and lower P, S scores for its templates (listed 15 in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa* These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egredios*) for our primers 'mcb398' and 'mcb869', 20 respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egredios* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 25 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

For further confirmation of universal nature of our primers, we blasted the sequence of our primers against the *mito* and *nr* databases of NCBI using BLAST software. The results of these analyses are shown in Tables 10, and 11, respectively.

30 Finally, the universal nature of the primers was tested in our laboratory with some more animal species listed in Table 12. These primers amplified all the animal species efficiently, giving rise to the band of expected size (472 bp). The results are shown in Figure 4. This experiments substantiated the results of P,S analysis and other *in-silico* analyses to show that the primers 'mcb398'and 'mcb 869' are universal primers.

The flow chart of establishing identity of the species of biological material of unknown animal origin using primers 'mcb398' and 'mcb869'



Examples

Example 1

Example for identification of a fragment of cytochrome b gene fulfilling the requirements of columns 1, 2 and 3 mentioned under sub-heading 'Objectives of invention' of heading

5 'Brief summary of invention'

The cytochrome b molecule has very vastly been used in molecular taxonomic studies.

Being a slow evolving gene, It has a tremendous information in its nucleotide sequences to distinguish the animals to their family, genus and species sources¹⁻⁶⁵. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in the *nr*

10 and *mito* databases of NCBI. We have explored these qualities of cytochrome b gene to establish the identity of confiscated remains of unknown animal origin to its family, genus and species sources. For this purpose, we have identified a fragment of cytochrome b gene which is highly polymorphic inter-specifically, however, it is monomorphic among the individual of same species, therefore it can group the individual of an unknown species

15 with the known individuals of reference species to which it belongs. In order to amplify this fragment from DNA isolated form any unknown origin, it was necessary that it remain flanked with the highly conserved sequences amongst a vast range of animal families. To identify such a unique fragment within the cytochrome b gene, we aligned the sequences of 221 distantly related animal species (listed in Table 1) representing various families using

20 software CLUSTAL X (1.8). These sequences were obtained from public database NCBI (<http://www.ncbi.nlm.nih.gov>). The aligned data was examined carefully for the conserved sites amongst all the species included in *in-silico* analysis. We identified a fragment (472 bp) of cytochrome b gene that was fulfilling all the requirements mentioned above and also under column 1, 2 and 3 of sub-heading 'Objectives of invention'.

25 As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are

30 characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antilope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

“taccatgaggacaataatctttgaggagaacagtcatcaccaatcccttcagcaatcccatacatcggtacaaaccttaga
atgaatctgaggagggtctcgttagataaagcaacccttacccgattttcgcccttccactttatcctccatttatcattgcagccct
accatagtgacacactgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaaattccattccac
5 ccctactacactatcaaagatactctaggagctactattaatttaaccctcatgctctagtcctattctcaccggacctgctggag
acccagacaactatacaccagcaaacccacttaatacaccccacatcaagcccgaatgatacttcctattgcatacgcaatcct
ccgatcaattctaacaaacttaggagg”

Example 2:

Example for development of universal primers to amplify the fragment identified mentioned under ‘Example 1’.

10

A pair of universal primer was designed which has the following features:

1. It targets the fragment identified (mentioned under ‘Example 1’) to amplify it in polymerase chain reaction (PCR).
2. Its 3’ and 5’ ends that are highly conserved (marked as star (*) in Table 2), amongst a vast range of animal species ensuring the amplification of the fragment mentioned above in a universal manner. The sequencing of the fragment amplified by these primes reveals the molecular signature of the species of analyzed material, which on comparison with the sequences of the known reference animals reveals the identity of the species of unknown biological material under investigation.
- 15 3. The tm (melting temperature) of both primers was almost similar (about 58 degree centigrade) ensuring the significant annealing of both the primers to its template, therefore significant amplification of targeted region in PCR.
- 20 4. The internal stability and P, S, score of the primers were ensured higher while designing it. The possibilities of internal loop formation, dimmer formation etc were also excluded by selecting its sequence uniquely. This ensured that the primer would be a good primer to be used in PCR for amplification of DNA from unknown animal origin.
- 25 5. The 3’ end of the primers were ensured to have either ‘G’ or ‘C’ to increase the probability of strong bonding at its 3’ends, which is necessary for efficient amplification of DNA template in PCR. It also strengthens the universal nature of the primer.
- 30 6. The sequences of the primers were ensured to be unique so that it does not give rise to non-specific and spurious products in PCR leading to confusion. It improved the efficiency and quality of the technique invented by us.

7. These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of *Antilope cervicapra*, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India.

5 8. The sequences of the universal primers invented are as follows:

Primers name	Sequence (5'-3')
'mcb398'	"TACCATGAGGACAAATATCATTCTG"
'mcb869'	"CCTCCTAGTTGTTAGGGATTGATCG"

10 **Example 3:**

Example for development of universal PCR conditions to ensure the amplification of a template of any unknown origin in PCR, hence strengthening the universal nature of the 15 technique invented by us

The PCR conditions developed had the following unique features:

1. These were capable of amplifying the DNA template of any animal origin in an 20 universal manner using the universal primers mentioned under 'Example 2'.

2. The conditions were selected to ensure the comparable annealing temperature for both the primers i.e. 'mcb398' and 'mcb869'.

25 3. The PCR conditions standardized herewith are universal; therefore, the possibility of PCR failure with a template of unknown origin due to non-standard conditions is excluded. It ensures the universal nature of our technique to be used in wildlife forensics.

4. The universal conditions mentioned above are:

Amplification reactions should be carried out in 20 µl reaction volume containing approximately 20 ng of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 30 1.5mM MgCl₂, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles should be held for 10 min.

Example 4:

Establishing the universal nature of our primer and experimental evidences to demonstrate the universal nature of primers:

The universal nature of the primers 'mcb398' and 'mcb 869' was ensured by the following

5 measures:

(a) Selecting the primers from the aligned cytochrome b gene sequences of 221 animal of distantly related species:

The cytochrome b gene sequences (1140 bp) were aligned using software *CLUSTAL X*

(1.8). The region of cytochrome b gene that was most conserved amongst 221 animal

10 species was selected to design the primers.

(b) Selecting the 3' and 5' ends of the primers at the highly conserved positions of cytochrome b gene:

The 3' and 5' ends of the primers were ensured to anneal to a highly conserved position

amongst 221 animal species representing a vast range of animal families. It was done to

15 ensure an efficient amplification of all the species in PCR. These positions are shown with

star (*) mark in Table 2.

(c) Ensuring either 'G' or 'C' at the 3' end of the primers:

It was ensured the primers to have either 'G' or 'C' at its 3' ends as these are the

nucleotides that ensure the strong bonding at the 3' ends of the primers due to three

20 hydrogen bonds while pairing with each other. The strong bonding at 3' ends helps the

primers to anneal properly with its template resulting in significant amplification in PCR.

(d) Selecting the sequences of the primers to ensure a higher internal stability, higher P, S score, and no primer dimmer and loop formation:

The sequences of the primers were selected to have a high P, S score for a vast range of

25 animal species (Shown in Table 1). The care was taken to exclude the possibilities of loop

or primer dimmer formation that could reduce the efficiency of the primers in PCR.

(e) Selecting the sequence of the primers with a comparable melting temperature:

The sequences of the primers were selected to have a comparable melting temperature so

that these could work together to amplify a DNA template in PCR at a similar annealing

30 temperature. The melting temperature of both the primers was about 58 degree centigrade

and the annealing temperature used in PCR is 51 degree centigrade.

Experimental evidences to demonstrate the universal nature of primers:

(1) Evidence from *In-silico* analysis :

(a) Selecting the primers within the most conserved region of mitochondrial cytochrome b gene

As mentioned above, the primers were designed to anneal within a highly conserved region of mitochondrial cytochrome b gene fragment of 472 bp. Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species representing a vast range of animal families. The conserved positions of nucleotide sequences are shown with star (*) mark in Table 2

Table 2 also demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico*. In the aligned sequences, the conserved nucleotides are marked with symbol (*). Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., 'Amplify (1.2)', 'Primer3' (<http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>) as well as manually.

(b) P, S, score analysis:

We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software *Amplify (1.2)*. The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98,63 (i.e. the situation where the primer has perfect match with template); however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S

score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S

score for one of the two primers were *Eumeces egregios* and *Equus ainus*. *Eumeces egregios* had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus ainus* was calculated as 91,61 and 73, 51 for 'mcb398'

and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair

(AFF= ^{5'}ctagtagaatgaatctgaggagg^{3'} and AFR= ^{5'}tatgcaaataggaatgtatcc^{3'}.) that have more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability

and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa*. These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in
5 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egreios*) for our primers 'mcb398' and 'mcb869', respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication
10 that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egreios* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

© BLAST analysis:

15 The sequences of primers 'mcb398' and 'mcb869' were blasted against mito and nr databases of NCBI to see its significant alignments with the sequences registered in GenBank. As expected, the most significant alignments of the sequences were found with the cytochrome b gene regions (within the 472 bp fragment mentioned in 'Example 1') of different animal species. This analysis also showed that the 3' as well as 5' ends of the
20 primers were highly conserved amongst a vast range of animal species, confirming the universal nature of the primers (Tables 10 and 11, respectively)

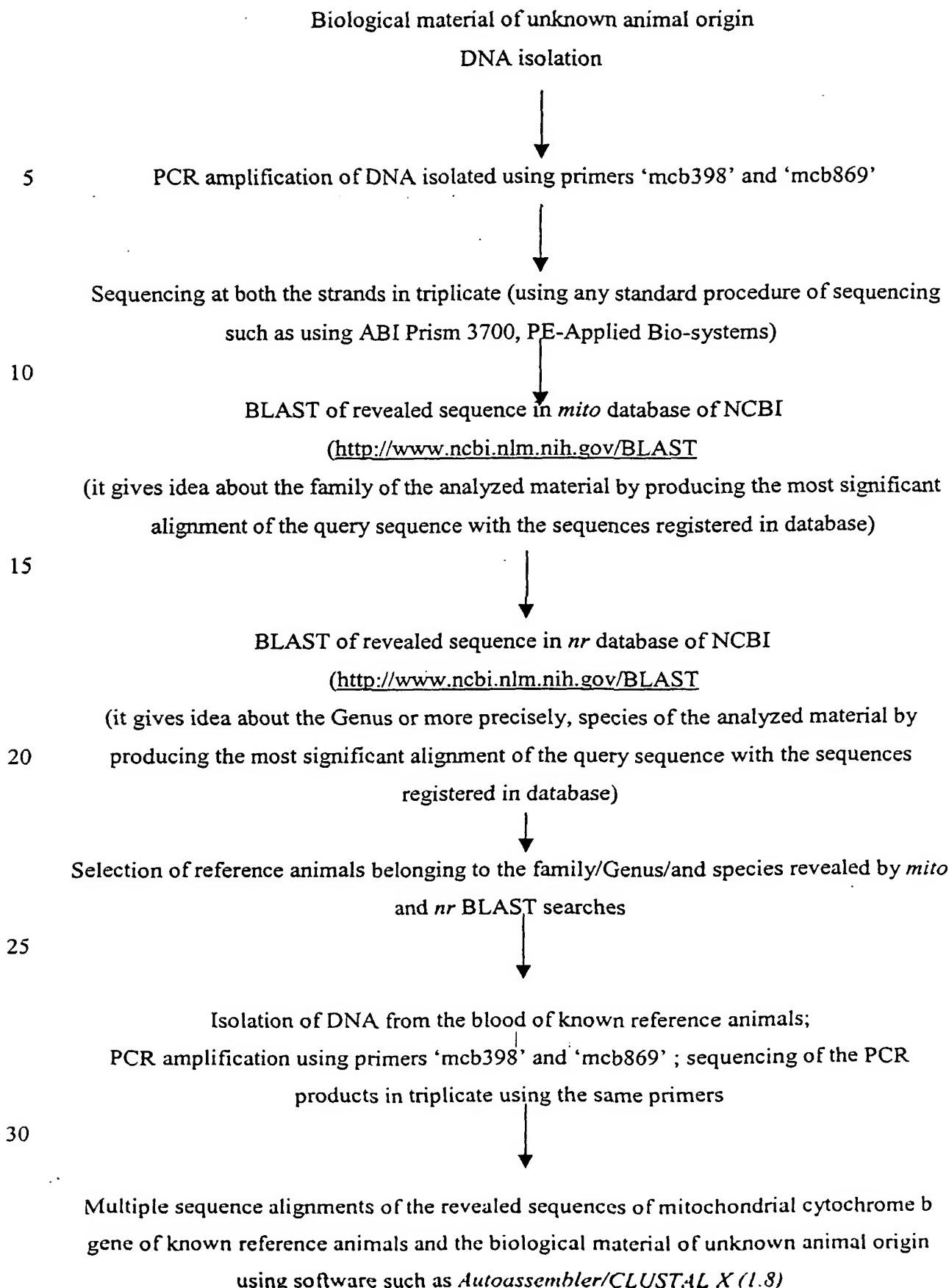
(2) Evidence from bench work/experiments done in laboratory conditions:

The DNA from different animals belonging to distantly related species (mentioned in
25 Table 12) was isolated and subjected to PCR amplification using the primers invented by us i.e. the primers 'mcb398' and 'mcb869'. The PCR products amplified were resolved in agarose gel by electrophoresis and visualized under UV light. The PCR products of expected size (472bp) were obtained from all the animals confirming the universal nature
30 of our primers. These results are shown in Figure 4.

Example 5:

Example to establish the identity of confiscated remains from unknown animal origin using the universal primers 'mcb398' and 'mcb869'.

The step-wise procedure to establish the identity of the biological material from an
35 unknown animal source is mentioned below:



↓

Identification of sequence from the aligned sequences
that is homologous (or significantly similar) to the cytochrome b gene sequence of the
DNA obtained from biological material of
5 unknown animal origin.
↓
The species of homologous sequence would be the species of the biological material under
10 investigation
↓
Application of the above information for the objectives mentioned in columns 7-13 under
sub-heading 'Objective of invention' of heading 'Summary of invention'

15 **Example 6:**

The actual execution of the technique invented

As a first application and to demonstrate the ease and utility of this method, we investigated a case of forensic identification submitted at our laboratory to seek scientific opinion on animal hunting evidence. In this case, we received the half burned remains of
20 an unknown animal, confiscated by the crime investigation agencies. The DNA was isolated from the above material following standard methods⁷⁴ and subjected to PCR amplification using the primers mentioned above (viz., 'mcb398' and 'mcb869'). Amplification reactions were carried out in 20 µl reaction volume containing 20 ng of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit
25 of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed were: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles was held for 10 min.

30 The PCR products obtained were sequenced in automated work station (ABI Prism 3700, PE-Biosystems) on both strands in triplicate and the sequence resolved (328 bp, shown in Figure 1a) was blasted against *mito* databases of NCBI using BLAST program⁷³. The most significant alignment (bits Value 365, E value e⁻¹⁰¹) of this sequence was produced with the cytochrome b gene sequence of *Felis catus*. (Table 3) indicating that species of

analyzed material belongs to family felidae. Further, the above sequence revealed from the confiscated remain was blasted against *nr* databases of NCBI using BLAST program. The most significant alignment (bits Value 603, E value e^{-170}) of this sequence was produced with the cytochrome b gene sequence of *Panthera pardus* (Table 4), indicating the identity
5 of the analyzed material as that of a *Panthera pardus* source. Based on this information, we selected the reference animals listed in Table 5 representing different species and subspecies of felidae. The DNA isolated from reference animals was amplified and sequenced on both strands in triplicate using the primer pair mentioned above. Consensus sequences obtained were aligned using program *CLUSTAL X (1.8)* (Table 6). Sequence
10 comparisons identified 113 variable sites in total amongst all animals analyzed (Table 7). Pair-vise comparisons of sequences were performed to find out the variation among different animals investigated. All the species investigated were differentiated by their unique nucleotides sequences. The molecular signatures of different reference animals were compared with the molecular signature of the confiscated skin 'adil.flesh'. Table 7
15 demonstrate that the maximum similarity of the adil.flesh with 'gz11' i.e. known Leopard (*Panthera pardus*) species, indicating the identity of the adil.flesh, the confiscated skin, as that of a *Panthera pardus* origin. We also calculated the similarity matrix showing the pair-vise similarity amongst the animal species under investigation using *PHYLIP* software. This matrix is shown in Table 8. It demonstrates that the animals belonging to different
20 species had more variation; however, the animals of same species had maximum similarity among their cytochrome b sequences. The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity with the sequences obtained from known Leopard source(99.7%, and 98.2 with 'gz11' and 'gz21', respectively); establishing the identity of the source of confiscated material as that of a Normal leopard (*Penthera pardus*) species. The step-vise procedure involved in above analysis is illustrated in Figure
25 1a, 1b and 1c, respectively.

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using BLAST software⁷³, it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. Application of the information revealed could be in
30

fulfilling the requirements of objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

The method of the invention can be used to establish the identity of confiscated animal

parts and products is one of the key requirements of wildlife identification in forensics. It

5 is needed to establish the crime with the criminal beyond a reasonable doubt to avoid the
human violation of wildlife resources. Various morphological biochemical and molecular

approaches have been given for this purpose; however, none of the current methods is
universally applicable to detect the mutilated animal remains of unknown origin. We have

10 identified a fragment on the mitochondrial cytochrome b gene, which has enormous
information to differentiate among various animal species back to the family, genus and

species sources. We have also found that this fragment is flanked by the highly conserved
sequences amongst a vast range of animal species. We invented a pair of universal primer

that can amplify this fragment of DNA isolated from the biological material of an
unknown animal origin in polymerase chain reaction (PCR) to reveal its identity at species

15 and sub-species sources. This novel invention has great potential to revolutionize the
whole scenario of wildlife forensic identification and crime investigation.

Table 1. The animal species included in the study for *in-silico* analysis

SN.	Code	Name	NCBI accession #	^a P,S/F	^b P,S/R
1	aep.mel	<i>Aepyceros melampus</i>	AF036289 ¹	97, 60	94, 62
2	ore.ore	<i>Oreotragus oreotragus</i>	AF036283 ¹	88, 52	94, 62
3	add.nas	<i>Addax nasomaculatus</i>	AF034722 ²	97, 60	95, 66
4	ory.dam	<i>Oryx damah</i>	AJ222685 ¹	90, 58	95, 66
5	hip.equ	<i>Hippotragus equinus</i>	AF022060 ³	98, 63	85, 55
6	alc.bus	<i>Alcelaphus buselaphus</i>	AJ222681 ¹	97, 60	98, 68
7	sig.lic	<i>Sigmooceros lichtensteinii</i>	AF034967 ⁴	97, 60	98, 68
8	bea.hun	<i>Beatragus hunteri</i>	AF034968 ⁴	97, 60	94, 62
9	dam.lun	<i>Damaliscus lunatus</i>	AF016635 ³	97, 60	77, 55
10	con.tau	<i>Connochaetes taurinus</i>	AF016638 ³	82, 56	93, 62
11	bis.bon	<i>Bison bonasus</i>	Y15005 ⁵	90, 58	87, 63
12	bos.gru	<i>Bos grunniens*</i>	AF091631 ⁶	90, 58	94, 62
13	bos.tra	<i>Bos tragocamelus*</i>	AJ222679 ¹	90, 58	95, 66
14	buba.bub	<i>Bubalus bubalis*</i>	D34637 ⁷	97, 60	93, 64
15	bub.min	<i>Bubalus mindorensis</i>	D82895 ⁸	97, 60	87, 62
16	tra.ang	<i>Tragelaphus angasii</i>	AF091633 ⁶	97, 60	87, 63
17	tra.eur	<i>Tragelaphus eurycerus</i>	AF036276 ¹	90, 58	97, 64
18	nem.cau	<i>Nemorhaedus caudatus*</i>	U17861 ⁹	95, 61	93, 59
19	pse.nay	<i>Pseudois nayaur</i>	AF034732 ²	89, 55	89, 59
20	amm.let	<i>Ammotragus lervia</i>	AF034731 ²	94, 58	97, 63
21	cap.fal	<i>Capra falconeri*</i>	D84202 ¹⁰	98, 63	95, 66
22	cap.ibe	<i>Capra ibex*</i>	AF034735 ²	98, 63	89, 58
23	hem.jem	<i>Hemitragus jemlahicus*</i>	AF034733 ²	95, 61	90, 61
24	rup.pyr	<i>Rupicapra pyrenaica</i>	AF034726 ²	95, 61	89, 59
25	rup.rup	<i>Rupicapra rupicapra</i>	AF034725 ²	95, 61	94, 64
26	pan.hod	<i>Pantholops hodgsoni</i>	AF034724 ²	98, 63	95, 66
27	bud.tax.tax	<i>Budorcas taxicolor taxicolor*</i>	U17868 ⁹	90, 58	95, 66
28	ovi.amm	<i>Ovis ammon*</i>	AF034727 ²	98, 63	97, 64
29	ovi.vig	<i>Ovis vignei*</i>	AF034729 ²	98, 63	97, 64
30	cap.cri	<i>Capcornis crispus*</i>	AJ304502 ¹¹	98, 63	94, 63
31	ovi.mos	<i>Ovibos moschatus</i>	U17862 ⁹	98, 63	92, 61
32	ore.ame	<i>Oreamnos americanus</i>	AF190632 ¹²	98, 63	94, 62
33	cep.dor	<i>Cephalophus dorsalis</i>	AF091634 ⁶	97, 58	90, 61
34	cep.max	<i>Cephalophus maxwellii</i>	AF096629 ¹³	97, 60	88, 53
35	alc.alc	<i>Alces alces</i>	AJ000026 ¹⁴	95, 61	93, 59
36	hyd.ine	<i>Hydropotes inermis</i>	AJ000028 ¹⁴	97, 60	90, 63
37	mun.mun	<i>Muntiacus muntjak*</i>	AF042718 ¹⁵	90, 58	93, 64
38	cer.ele.kan	<i>Cervus elaphus kansuensis*</i>	AB021098 ¹⁶	98, 63	82, 59
39	cer.ele.xan	<i>Cervus elaphus xanthopygus*</i>	AB021097 ¹⁶	98, 63	82, 59
40	cer.ele.can	<i>Cervus elaphus canadensis*</i>	AB021096 ¹⁶	98, 63	90, 61
41	cer.nip.ce	<i>Cervus nippon centralis</i>	AB021094 ¹⁶	98, 63	90, 61
42	cer.nip.ye	<i>Cervus nippon yesoensis</i>	AB021095 ¹⁶	98, 63	90, 61
43	cer.nip.ke	<i>Cervus nippon keramae</i>	AB021091 ¹⁶	98, 63	90, 61

44 cer.nip.pu	<i>Cervus nippon pulchellus</i>	AB021090 ¹⁶	98, 63	90, 61
45 cer.nip.ni	<i>Cervus nippon nippon</i>	AB021093 ¹⁶	98, 63	90, 61
46 cer.elas.	<i>Cervus elaphus scoticus</i>	AB021099 ¹⁶	98, 63	90, 61
47 cer.dam	<i>Cervus dama</i>	AJ000022 ¹⁴	98, 63	88, 53
48 ran.tar	<i>Rangifer tarandus</i>	AJ000029 ¹⁴	98, 63	89, 57
49 mos.fus	<i>Moschus fuscus*</i>	AF026883 ¹⁷	90, 59	90, 61
50 mos.leu	<i>Moschus leucogaster*</i>	AF026883 ¹⁷	90, 59	90, 61
51 mos.chr	<i>Moschus chrysogaster*</i>	AF026887 ¹⁷	90, 59	90, 61
52 mos.ber	<i>Moschus berezovskii*</i>	AF026886 ¹⁷	90, 59	90, 61
53 mos.mos	<i>Moschus moschiferus*</i>	AF026883 ¹⁷	90, 59	92, 61
54 kob.ell	<i>Kobus ellipsiprymnus</i>	AF022059 ³	91, 61	95, 66
55 kob.meg	<i>Kobus megaceros</i>	AJ222686 ¹	91, 61	83, 56
56 red.aru	<i>Redunca arundinum</i>	AF096628 ¹³	91, 61	94, 62
57 red.ful	<i>Redunca fulvorufa</i>	AF036284 ¹	89, 57	94, 62
58 neo.mos	<i>Neotragus moschatus</i>	AJ222683 ¹	89, 57	94, 62
59 pel.cap	<i>Pelea capreolus</i>	AF022055 ³	91, 61	90, 61
60 ant.cer	<i>Antilope cervicapra*</i>	AF022058 ³	82, 56	93, 64
61 sai.tat	<i>Saiga tatarica</i>	AF064487 ¹⁸	91, 61	92, 61
62 gaz.dam	<i>Gazella dama</i>	AF025954 ³	91, 61	92, 61
63 our.out	<i>Ourebia ourebi</i>	AF036288 ¹	82, 56	82, 59
64 gaz.gaz	<i>Gazella gazella*</i>	AJ222682 ¹	91, 61	89, 57
65 rap.mel	<i>Raphicerus melanotis</i>	AF022053 ³	81, 54	80, 50
66 mad.kir	<i>Madoqua kirkii</i>	AF022070 ³	90, 58	97, 65
67 ant.ame	<i>Antilocapra americana</i>	AF091629 ⁶	98, 63	98, 68
68 tra.jav	<i>Tragulus javanicus*</i>	D32189 ¹⁹	86, 57	86, 59
69 tra.nap	<i>Tragulus napu*</i>	X56288 ²⁰	81, 52	93, 58
70 bal.acu	<i>Balaenoptera acutorostrata</i>	X75753 ²¹	89, 56	97, 61
71 bal.bon	<i>Balaenoptera bonaerensis</i>	X75581 ²¹	89, 56	93, 59
72 bal.bor	<i>Balaenoptera borealis*</i>	X75582 ²¹	89, 56	93, 59
73 bal.edi	<i>Balaenoptera edeni</i>	X75583 ²¹	89, 56	88, 54
74 esc.rob	<i>Eschrichtius robustus*</i>	X75585 ²¹	97, 61	86, 57
75 bal.mus	<i>Balaenoptera musculus*</i>	NC_001601 ²²	97, 57	93, 59
76 meg.nov	<i>Megaptera novaeangliae*</i>	X75584 ²¹	97, 61	94, 63
77 bal.phy	<i>Balaenoptera physalus*</i>	NC_001321 ²²	97, 57	94, 63
78 cap.mar	<i>Caperea marginata</i>	X75586 ²¹	93, 55	91, 53
79 cep.com	<i>Cephalorhynchus commersonii</i>	AF084073 ²⁴	85, 51	88, 55
80 cep.eut	<i>Cephalorhynchus eutyropis*</i>	AF084072 ²⁴	85, 51	92, 59
81 lag.obl	<i>Lagenorhynchus obliquidens</i>	AF084067 ²⁴	94, 59	92, 59
82 cep.hec	<i>Cephalorhynchus heavisidii</i>	AF084070 ²⁴	89, 56	97, 63
83 cep.hec	<i>Cephalorhynchus hectori*</i>	AF084071 ²⁴	89, 56	92, 59
84 lag.aus	<i>Lagenorhynchus australis</i>	AF084069 ²⁴	86, 54	92, 59
85 lag.cru	<i>Lagenorhynchus cruciger</i>	AF084068 ²⁴	86, 54	92, 59
86 lag.obs	<i>Lagenorhynchus obscurus</i>	AF084066 ²⁴	86, 54	92, 59
87 lis.bor	<i>Lissodelphis borealis</i>	AF084064 ²⁴	85, 51	92, 59
88 lis.per	<i>Lissodelphis peronii</i>	AF084065 ²⁴	86, 54	92, 59
89 glo.mac	<i>Globicephala macrorhynchus</i>	AF084055 ²⁴	94, 59	88, 55
90 glo.mel	<i>Globicephala melas</i>	AF084056 ²⁴	94, 59	88, 55
91 fer.att	<i>Feresa attenuata*</i>	AF084052 ²⁴	94, 59	92, 59

92 pep.ele	<i>Peponocephala elecra</i> *	AF084053 ²⁴	94, 59	88, 55
93 gra.gri	<i>Grampus griseus</i>	AF084059 ²⁴	97, 61	89, 59
94 pse.cra	<i>Pseudorca crassidens</i> *	AF084057 ²⁴	94, 59	92, 59
95 lag.acu	<i>Lagenorhynchus acutus</i>	AF084075 ²⁴	98, 63	89, 59
96 orci.bre	<i>Orcinus orca</i>	AF084061 ²⁴	86, 57	82, 52
97 orca.bre	<i>Orcaella brevirostris</i>	AF084063 ²⁴	86, 57	91, 54
98 del.cap	<i>Delphinus capensis</i>	AF084087 ²⁴	96, 54	97, 63
99 del.tro	<i>Delphinus tropicalis</i>	AF084088 ²⁴	97, 57	97, 63
100 del.del	<i>Delphinus delphis</i>	AF084085 ²⁴	97, 57	97, 63
101 sten.cly	<i>Stenella clymene</i>	AF084083 ²⁴	97, 57	97, 63
102 sten.coe	<i>Stenella coeruleoalba</i>	AF084082 ²⁴	97, 57	97, 66
103 tur.adu	<i>Tursiops aduncus</i>	AF084092 ²⁴	97, 57	97, 63
104 sten.fro	<i>Stenella frontalis</i>	AF084090 ²⁴	97, 57	97, 63
105 saus.chi	<i>Sousa chinensis</i>	AF084080 ²⁴	97, 57	88, 59
106 sten.lon	<i>Stenella longirostris</i>	AF084103 ²⁴	97, 61	97, 63
107 turs.tru	<i>Tursiops truncatus</i>	AF084095 ²⁴	97, 57	96, 59
108 lage.alb	<i>Lagenorhynchus alborostris</i>	AF084074 ²⁴	97, 61	97, 66
109 sten.bre	<i>Steno bredanensis</i>	AF084077 ²⁴	97, 61	94, 64
110 sota.flu	<i>Sotalia fluviatilis</i>	AF304067 ²⁵	97, 61	97, 63
111 del.leu	<i>Delphinapterus leucas</i>	U72037 ²⁶	97, 61	95, 66
112 mono.mon	<i>Monodon monoceros</i>	U72038 ²⁶	97, 61	95, 66
113 plat.gan	<i>Platanista gangetica</i> *	AF304070 ²⁵	97, 61	86, 59
114 plat.min	<i>Platanista minor</i> *	X92543 ²⁷	97, 61	86, 59
115 kogi.bre	<i>Kogia breviceps</i>	U72040 ²⁶	97, 59	90, 63
116 kogi.sim	<i>Kogia simus</i>	AF304072 ²⁵	96, 55	92, 63
117 phys.cat	<i>Physeter catodon</i>	AF304073 ²⁵	97, 57	80, 58
118 lipo.vex	<i>Lipotes vexillifer</i> *	AF304071 ²⁵	89, 56	88, 53
119 phoc.sin	<i>phocoena sinus</i>	AF084051 ²⁴	87, 49	92, 62
120 bera.bai	<i>Berardius bairdii</i>	X92541 ²⁷	96, 55	90, 59
121 ziph.car	<i>Ziphius cavirostris</i>	X92540 ²⁷	97, 61	89, 57
122 meso.eur	<i>Mesoplodon europaeus</i>	X92537 ²⁷	97, 57	90, 61
123 meso.bid	<i>Mesoplodon bidens</i>	X92538 ²⁷	97, 61	92, 61
124 meso.den	<i>Mesoplodon densirostris</i>	X92536 ²⁷	91, 61	94, 63
125 hype.amp	<i>Hyperoodon ampullatus</i> *	X92539 ²⁷	97, 61	90, 65
126 meso.per	<i>Mesoplodon peruvianus</i>	AF304074 ²⁵	97, 61	86, 58
127 pont.blia	<i>Pontoporia blainvilliei</i>	AF304069 ²⁵	92, 59	88, 55
128 hipp.amp	<i>Hippopotamus amphibius</i>	Y08813 ²⁹	92, 58	95, 66
129 hex.lib	<i>Hexaprotodon liberiensis</i>	Y08814 ²⁹	98, 63	97, 66
130 rhin.son	<i>Rhinoceros sondaicus</i> *	AJ245723 ¹⁰	90, 59	87, 61
131 cera	<i>Ceratotherium simum</i>	NC_00180S ¹¹	90, 59	90, 63
132 dic.sum	<i>Dicerorhinus sumatrensis</i>	AJ245723 ¹⁰	90, 59	86, 57
133 equu	<i>Equus asinus</i>	NC_0017SS ¹¹	91, 61	73, 51
134 baby.bab	<i>Babyrousa babyrussa</i>	Z50106 ¹¹	89, 56	85, 56
135 phac.afr	<i>Phacochoerus africanus</i>	Z50090 ¹¹	90, 59	87, 54
136 sus.scr.ew	<i>Sus scrofa</i> haplotype EWBJ*	AF136549 ¹⁴	97, 57	83, 54
137 sus.bar	<i>Sus barbatus</i>	Z50107 ¹¹	97, 57	85, 55
138 lama.gla	<i>Lama glama</i>	U06429 ¹¹	89, 55	85, 53
139 lama.gua	<i>Lama guanicoe</i>	Y08812 ²⁹	88, 54	86, 57

140	vic.vic	<i>Vicugna vicugna</i>	U06430 ³⁵	89, 55	85, 53
141	cam.bac	<i>Camelus bactrianus</i>	U06427 ³⁵	94, 58	86, 58
142	arc.for	<i>Arctocephalus forsteri</i>	XS2293 ³⁶	97, 60	87, 64
143	arc.gaz	<i>Arctocephalus gazella</i>	X82292 ³⁶	94, 58	87, 64
144	eum.jub	<i>Eumetopias jubatus</i>	X82311 ³⁶	97, 57	86, 57
145	zal.cal	<i>Zalophus californianus</i>	X82310 ³⁶	89, 55	86, 57
146	odo.ros	<i>Odobenus rosmarus</i>	X82299 ³⁶	91, 61	81, 52
147	pho.vit	<i>Phoca vitulina</i>	X82306 ³⁶	90, 58	87, 64
148	pho.fascia	<i>Phoca fasciata</i>	X82302 ³⁶	98, 63	95, 66
149	pho.gro	<i>Phoca groenlandica</i>	X82303 ³⁶	92, 59	90, 61
150	cys.cri	<i>Cystophora cristata</i>	X82294 ³⁶	89, 56	87, 64
151	hyd.lep	<i>Hydrurga leptonyx</i>	X82297 ³⁶	89, 55	82, 54
152	lep.wed	<i>Leptonychotes weddelli</i>	X72005 ³⁷	98, 63	91, 66
153	mir.leo	<i>Mirounga leonina</i>	X82298 ³⁶	89, 55	82, 59
154	eri.bar	<i>Erignathus barbatus</i>	X82295 ³⁶	89, 56	87, 63
155	mon.sch	<i>Monachus schauinslandi</i>	X72209 ³⁷	91, 61	87, 60
156	hela.mal	<i>Helarctos malayanus*</i>	U18899 ³⁸	84, 54	90, 63
157	sel.thi	<i>Selenarctos thibetanus*</i>	AB020910 ³⁹	89, 57	87, 64
158	ail.ful	<i>Ailurus fulgens*</i>	X94919 ⁴⁰	93, 55	87, 64
159	fel	<i>Felis catus</i>	NC_001700 ⁴¹	85, 56	90, 63
160	can	<i>Canis familiaris</i>	NC_002008 ⁴²	98, 58	84, 54
161	tal	<i>Talpa europaea</i>	NC_002391 ⁴³	81, 50	92, 57
162	gla.sab	<i>Glaucomys sabrinus</i>	AF011738 ⁴⁴	90, 59	82, 54
163	gla.vol	<i>Glaucomys volans</i>	AB030261 ⁴⁵	90, 59	87, 60
164	hyl.pha	<i>Hylopetes phayrei*</i>	AB030259 ⁴⁵	91, 61	81, 50
165	pet.set	<i>Petinomys setosus*</i>	AB030260 ⁴⁵	91, 61	81, 50
166	bel.pea	<i>Belomys pearsonii*</i>	AB030262 ⁴⁵	91, 61	87, 64
167	pte.mom	<i>Pteromys momonga*</i>	AB030263 ⁴⁵	97, 61	90, 63
168	gala.demi	<i>Galagooides demidoff</i>	AF271411 ⁴⁶	97, 58	87, 64
169	pero.pot	<i>Perodicticus potto</i>	AF271413 ⁴⁶	97, 60	87, 63
170	gala.mat	<i>Galago matschiei</i>	AF271409 ⁴⁶	97, 60	90, 61
171	gala.moh	<i>Galago moholi</i>	AF271410 ⁴⁶	97, 57	95, 66
172	oto.gar	<i>Otolemur garnettii</i>	AF271412 ⁴⁶	92, 58	87, 60
173	lor.tar	<i>Loris tardigradus*</i>	US3581 ⁴⁷	97, 60	93, 59
174	nyc.cou	<i>Nycticebus coucang*</i>	US3580 ⁴⁷	97, 60	95, 66
175	mus	<i>Mus musculus</i>	NC_001569 ⁴⁸	97, 60	86, 59
176	gorr	<i>Gorilla gorilla</i>	NC_001645 ⁴⁹	89, 57	80, 58
177	homo	<i>Homo sapiens sapiens</i>	NC_001807 ⁵⁰	96, 55	84, 64
178	dug.dug	<i>Dugong dugong*</i>	U07564 ⁵¹	97, 60	89, 59
179	ele.max	<i>Elephas maximus*</i>	AB002412 ⁵²	97, 60	76, 57
180	afr.con	<i>Afropavo congensis</i>	AF013760 ⁵³	97, 58	87, 63
181	pavo.mut	<i>Pavo muticus*</i>	AF013763 ⁵³	97, 57	87, 63
182	tra.bly	<i>Tragopan blythii*</i>	AF200722 ⁵⁴	89, 55	85, 57
183	tra.sat	<i>Tragopan satyra*</i>	AF229837 ⁵⁴	89, 55	86, 61
184	tra.cob	<i>Tragopan caboti</i>	AF200723 ⁵⁴	89, 55	86, 61
185	tra.tem	<i>Tragopan temminckii*</i>	AF023802 ⁵⁵	89, 55	81, 56
186	arg.arg	<i>Argusianus argus</i>	AF013761 ⁵⁵	89, 55	87, 63
187	cat.wal	<i>Catrcus wallichii*</i>	AF023792 ⁵⁵	88, 54	85, 57

188 cro.cro	<i>Crossoptilon crossoptilon</i> *	AF028794 ⁵³	89, 55	85, 57
189 sym.ree	<i>Syrmaticus reevesi</i> *	AF028301 ⁵³	89, 55	85, 57
190 bam.tho	<i>Bambusicola thoracica</i> *	AF028790 ⁵³	80, 48	94, 64
191 fra.fra	<i>Francolinus francolinus</i>	AF013762 ⁵³	97, 58	86, 61
192 ith.cru	<i>Ithaginis cruentus</i> *	AF068193 ⁵³	98, 63	85, 57
193 ant.par	<i>Anthropoides paradisea</i>	U27557 ⁵⁶	85, 56	82, 58
194 ant.vir	<i>Anthropoides virgo</i>	U27545 ⁵⁶	84, 54	82, 52
195 gru.ant.an	<i>Grus antigone antigone</i>	U11060 ⁵⁷	90, 53	87, 63
196 gru.ant.gi	<i>Grus antigone gillae</i>	U11064 ⁵⁷	90, 53	87, 63
197 gru.any.sh	<i>Grus antigone sharpei</i>	U11061 ⁵⁷	90, 58	87, 63
198 gru.leu	<i>Grus leucogeranus</i> *	U27549 ⁵⁶	90, 53	87, 63
199 gru.can.pr	<i>Grus canadensis pratensis</i>	U27553 ⁵⁶	97, 60	87, 63
200 gru.can.ro	<i>Grus canadensis rowani</i>	U27552 ⁵⁶	97, 60	87, 63
201 gru.can.ta	<i>Grus canadensis tabida</i>	U27551 ⁵⁶	98, 63	87, 63
202 gru.can.ca	<i>Grus canadensis canadensis</i>	U27554 ⁵⁶	97, 61	87, 63
203 gru.ame	<i>Grus americana</i>	U27555 ⁵⁶	90, 53	87, 63
204 gru.gru	<i>Grus grus</i>	U27546 ⁵⁶	89, 54	87, 63
205 gru.mon	<i>Grus monacha</i> *	U27548 ⁵⁶	90, 58	87, 63
206 gru.nig	<i>Grus nigricollis</i> *	U27547 ⁵⁶	90, 58	87, 63
207 gru.jap	<i>Grus japonensis</i>	U27550 ⁵⁶	81, 54	87, 63
208 cic.boy	<i>Ciconia boyciana</i> *	NC_002196 ⁵⁸	94, 58	79, 60
209 rhe.ame	<i>Rhea americana</i>	AF090339 ⁵⁹	93, 63	79, 60
210 ant.alb	<i>Anthracoboceros albirostris</i> *	U89190 ⁶⁰	97, 61	86, 59
211 fal.fam	<i>Falco femoralis</i>	U83310 ⁶¹	97, 61	86, 60
212 fal.ver	<i>Falco verpertinus</i>	U83311 ⁶¹	97, 61	85, 57
213 fal.par	<i>Falco peregrinus</i> *	U83307 ⁶¹	97, 61	84, 52
214 fal.spa	<i>Falco sparverius</i>	U83306 ⁶¹	92, 59	80, 51
215 ayt.ame	<i>Aythya americana</i>	NC_000877 ⁶²	98, 63	94, 62
216 smi.sha	<i>Smithornis sharpei</i>	NC_000879 ⁵⁹	97, 58	90, 61
217 vid.cha	<i>Vidua chalybeata</i>	NC_000880 ⁵⁹	97, 60	87, 64
218 chry.pic	<i>Chrysemys picta</i>	NC_002073 ⁶³	89, 56	86, 57
219 emy.orb.ku	<i>Emys orbicularis</i>	AJ131425 ⁶⁴	90, 59	94, 63
220 che.mud	<i>Chelonia mydas</i> *	AB012104 ⁶³	90, 58	94, 63
221 eum.egf	<i>Eumeces elegans</i>	AB016606 ⁶³	86, 55	73, 51

Table 2. Multiple sequence alignment of 471 bp fragment of mitochondrial cytochrome b gene of 221 animal species

PRIMER 'mcB393'	TACCATGAGGACAAATATCATTCTG TGCCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACAAATCTCTCTCAGCAA 60
aep.mel	TTCCGTGAGGACAAATATCATTCTGAGGGGCTACAGTCATTACTAAATCTCTCTCAGCAA 60
ore.ore	TGCCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
add.nas	TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTTATCACTAACCTCTCTCAGCAA 60
cry.dam	TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
hip.equ	TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
alc.bus	TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
sig.lis	TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
bea.hun	TGCCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
dam.lun	TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
con.tau	TACCATGAGGACAAATATCCTTTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
amm.ler	TGCCATGAGGACAGATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
pse.nay	TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
cap.ibe	TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
hem.jem	TACCATGAGGACAGATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
cap.fal	TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
rup.pyr	TACCATGAGGACAGATATCATTCTGAGGGAGCAACAGTTATTACCAACCTCTCTCAGCAA 60
rup.sup	TACCATGAGGACAGATATCATTCTGGGGAGCAACAGTTATTACCAACCTCTCTCAGCAA 60
nem.cau	TACCATGAGGACAGATATCATTCTGAGGGGGCAACAGTTATTACCAACCTCTCTCAGCAA 60
bud.tax.tax	TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
pan.hod	TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
ovi.amm	TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
ovi.vig	, TACCATGAGGACAAATATCATTCTGAGGGGGCTACAGTCATTACTAAACCTCTCTCAGCAA 60
cap.cri	TACCATGAGGACAAATATCATTCTGAGGGGGCTACAGTCATTACTAAACCTCTCTCAGCAA 60
ovi.mos	TACCATGAGGACAAATATCATTCTGAGGGAGCTACAGTCATTACCAACCTCTCTCAGCAA 60
ore.ame	TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
cep.dor	TCCCATGAGGGCAAAATATCATTCTGAGGGAGCCACAGTCATTACCAACCTCTCTCAGCAA 60
cep.max	TCCCATGAGGGCAAAATATCATTCTGAGGGAGCCACAGTCATTACCAACCTCTCTCAGCAA 60
bis.bon	TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
bos.gru	TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
bos.cra	TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
bub.min	TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
buba.bub	TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
tra.ang	TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
tra.eur	TACCATGAGGACAAATATCCTTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
kob.ell	TACCATGAGGACAAATATCCTTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
kob.meg	TACCATGAGGACAAATATCCTTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
zed.aru	TACCATGAGGACAAATATCCTTCTGAGGGAGCAACAGTTATCACTAACTCTCTCAGCAA 60
zed.ful	TGCCATGGGCACAAAATATCCTTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
neo.mos	TGCCATGGGCACAAAATATCCTTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
pel.cap	TACCATGAGGACAAATATCCTTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
gaz.dam	TACCATGAGGACAAATATCCTTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
out.out	TACCATGAGGACAAATATCCTTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
ant.cer	TACCATGAGGACAAATATCCTTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
sai.tai	TACCATGAGGACAAATATCCTTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCAGCAA 60
mai.kis	TGCCATGGGCACAAAATATCCTTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
gap.mel	TACCATGGGCACAAAATATCCTTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
gap.gac	TACCATGGGCACAAAATATCCTTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
ant.ame	TACCATGGGCACAAAATATCCTTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
hyd.lne	TTCCATGGGCACAAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
mun.mun	TACCATGGGCACAAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
alc.alb	TACCATGGGCACAAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60
cer.elk.kun	TACCATGGGCACAAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTCTCTCAGCAA 60

cer.elo.xan	TACCATGAGGACAAATATCATTCTGAGGAGCAACCGTCATTACCAACCTTCTCAGCAA	60
cer.elo.can	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCAGCAA	60
cer.nip.cent	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCAGCAA	60
cer.nip.yes	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCAGCAA	60
cer.nip.ker	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCAGCAA	60
cer.nip.pul	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCAGCAA	60
cer.nip.nip	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCAGCAA	60
cer.elo.sco	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCAGCAA	60
cer.dam	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTCTCAGCAA	60
ran.tar	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTCTCAGCAA	60
mos.fus	TACCTTGAGGACAAATATCTTCTGAGGAGCGACAGTTATTACCAATCTCTCAGCAA	60
mos.leu	TACCTTGAGGACAAATATCTTCTGAGGAGCAACAGTTATTACCAATCTCTCAGCAA	60
mos.chr	TACCTTGAGGACAAATATCTTCTGAGGAGCAACAGTTATTACCAATCTCTCAGCAA	60
mos.ber	TACCTTGAGGACAAATATCTTCTGAGGAGCAACAGTTATTACCAATCTCTCAGCAA	60
mos.mos	TACCTTGAGGACAAATATCTTCTGAGGAGCAACAGTCATCACTAACCTCTCAGCAA	60
tra.jav	TACCCCTGAGGAGCAGATACTTTCTGAGGAGCACAGTCATCACCAACCTCTTATCAGCTA	60
trag.nap	TACCCCTGAGGGCAAATATCTTTTGAGGAGCTACAGTCATCACTAACCTCTTCTCAGCAA	60
bala.acu	TACCCCTGAGGACAAATATCATTGTAGGTGCAACCGTCATCACCAACCTCTTATCAGCAA	60
bala.bon	TACCCCTGAGGACAAATATCATTGTAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
bala.bor	TACCCCTGAGGACAAATATCATTGTAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
bala.edi	TACCCCTGAGGACAAATATCATTGTAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
esch.rob	TACCCCTGAGGACAAATATCATTGTAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
bala.mus	TGCCCTGAGGACAAATATCATTCTGAGGAGCAACCGTCATCACCAACCTCTTATCAGCAA	60
mega.nov	TACCCCTGAGGACAAATATCATTCTGAGGAGCAACCGTCATCACCAACCTCTTATCAGCAA	60
bala.phy	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACTGTAATCACTAACCTCTTATCAGCAA	60
cap.mar	TGCCCTGAGGACAGATACTTTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA	60
ceph.com	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
ceph.eut	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
lage.obl	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
ceph.hea	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
ceph.hec	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
lage.aus	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
lage.cru	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
lage.obs	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
lisso.bor	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
lisso.per	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
glo.mac	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
glo.mel	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
fere.att	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
pepo.ele	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
gram.gri	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
pse.cra	TACCCCTGGGGACAGATACTTTTGAGGTGCAACAGTCATCACCAACCTCTTATCAGCAA	60
lage.acu	TACCATGAGGACAAATATCATTCTGAGGCGAACCGTTATCACCAATCTCTTATCAGCAA	60
orti.bre	TACCCCTGAGGACAGATACTTTCTGAGGCGAACCGTCATTACTAATCTCTTATCAGCAA	60
crca.bre	TACCCCTGAGGACAGATACTTTCTGAGGCGAACCGTCATCACCAATCTCTTATCAGCAA	60
del.cap	TGCCCTGGGGACAAATATCATTCTGAGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
del.tro	TGCCCTGGGGACAAATATCATTCTGAGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
del.del	TGCCCTGGGGACAAATATCATTCTGAGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
sten.oly	TGCCCTGGGGACAAATATCATTCTGAGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
sten.coe	TGCCCTGGGGACAAATATCATTCTGAGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
tur.adu	TGCCCTGGGGACAAATATCATTCTGAGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
sten.fro	TGCCCTGGGGACAAATATCATTCTGAGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
saus.chi	TGCCCTGGGGACAAATATCATTCTGAGGCGAACCGTTATCACCAACCTCTTATCAGCAA	60
sten.lon	TACCCCTGAGGACAAATATCATTCTGAGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
turs.tru	TGCCCTGGGGACAAATATCATTCTGAGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
lage.alb	TACCCCTGAGGACAAATATCATTCTGAGGCGAACCGTCATCACTAATCTCTTATCAGCAA	60
sten.bre	TACCCCTGAGGACAAATATCATTCTGAGGCGAACCGTCATTACCAACCTCTTATCAGCAA	60
sota.flu	TACCCCTGAGGACAAATATCATTCTGAGGCGAACCGTCATTACCAACCTCTTATCAGCAA	60

del.leu	TACCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATTACCAATCTCCTATCAGCAA 60
mono.mon	TACCCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA 60
plat.gan	TACCCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTTATCAGCAA 60
plat.min	TACCCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTTATCAGCAA 60
kogi.bre	TACCCCTGAGGCCAAATATCATTCTGAGGGAGCAACCGTCATCACCAACCTTATCCGCAA 60
kogi.sim	TGCCCTGAGGCCAAATATCATTCTGAGGGAGCAACCGTCATCACAAACCTTATCCGCAA 60
phys.cat	TGCCCTGAGGACAAATATCATTCTGAGCCGCAACCGTTATCACAAACCTTCTATCAGCAA 60
lipo.vex	TACCCCTGAGGACAAATATCATTGAGGGCGAACCGTCATCACTAATCTTCTATCAGCAA 60
phoc.sin	TGCCCTGGGGACAAATATCATTGAGGTGCTACCGTCATCACAAACCTCTTATCAGCAA 60
bera.bai	TGCCCTGAGGCCAAATATCATTCTGAGGTGCAACCGTCATCACAAACCTCTTATCCGCTA 60
ziph.car	TACCTTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACAAACCTTATCCGCTA 60
meso.eur	TTCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTTATTACCAACCTCTTATCCGCAA 60
meso.bid	TACCCCTGAGGACAAATATCATTCTGAGGGCGAACCTGTTATTACTAACCTCCTATCCGCTA 60
meso.den	TACCATGAGGACAAATATCCTTCTGAGGTGCAACTGTCAATTACCAATCTTCTATCCGCTA 60
hype.amp	TACCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAATCTCCTATCCGCAA 60
meso.per	TACCTTGAGGACAAATATCATTCTGAGGGCGAACCTGCTATTACTAACCTTATCTGCTA 60
pont.bla	TACCCCTGAGGACAAATATGTCATTCTGAGGTGCCACTGTCACTAACCTCCTATCAGCGA 60
hex.lib	TACCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAACTTACTATCAGCTA 60
hipp.amp	TGCCATGAGGACAAATGTCAATTCTGAGGGGCAACAGTCATTACCAACTCTGTCACTA 60
dic.sum	TACCATGAGGTCAAATATCCTTCTGAGGGAGCCACAGTTATCACAAATCTCCTCTCAGCCA 60
rhin.scn	TACCATGAGGTCAAATATCCTTCTGAGGGGCTACAGTCATTACAAATCTCCTCTCAGCCA 60
cera	TACCATGAGGCCAAATATCCTTCTGAGGGGCTACAGTCATTACAAACCTCCTCTCAGCTA 60
equu	TACCATGAGGACAAATATCCTTCTGAGGGAGCAACGGTCATTACAAACCTCCTATCAGCAA 60
baby.bab	TACCTTGAGGACAAATATCATTGAGGGAGCTACCGTCATTACAAACCTACTATCAGCCA 60
phac.afr	TACCCCTGAGGACAAATATCGTTCTGAGGGAGCCACAGTCATCACAAACCTACTATCAGCCA 60
sus.bar	TGCCCTGAGGACAAATATCATTCTGAGGGAGCTACGGTCATCACAAATCTACTATCAGCTA 60
sus.scr.ewb3	TGCCCTGAGGACAAATATCATTCTGAGGGAGCTACGGTCATCACAAATCTACTATCAGCTA 60
lama.gla	TCCCCTGAGGACAAATATCATTGAGGGGCAACAGTAATTACAAATCTACTCTCGGCCA 60
lama.gua	TCCCCTGAGGCCAAATATCATTGAGGGGCAACAGTAATTACAAACCTACTCTCGGCCA 60
vic.vic	TCCCCTGAGGACAAATATCATTGAGGGGCAACAGTAATTACAAACCTACTCTCAGCAA 60
cam.bac	TCCCCTGAGGACAGATATCATTCTGGGGAGCAACAGTAATTACCAACCTACTCTCAGCAA 60
arc.for	TTCCCATGAGGACAAATATCATTCTGAGGGAGCGACCGTCATTACCAACCTCCTATCAGCAG 60
arc.gaz	TTCCCATGAGGACAGATATCATTCTGAGGGAGCAACCGTCATTACCAACCTCCTGTCACTA 60
eum.jub	TTCCGTGAGGACAAATATCATTCTGAGGGAGCAACCGTCATTACCAACCTCCTATCAGCTA 60
zal.cal	TTCCCATGAGGACAAATATCATTGAGGGAGCAACCGTCATTACCAACCTCCTATCAGCAG 60
odo.ros	TACCATGAGGACAAATATCCTTCTGAGGGAGCAACCGTCATCACCAACCTTCTGTCACTA 60
pho.fasciata	TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATCACAAACCTTCTGTCACTA 60
pho.gro	TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATCACAAATCTACTATCAGCAA 60
pho.vit	TACCATGAGGCCAAATATGTCATTCTGAGGGAGCAACAGTTATCCTAATCTACTATCAGCAA 60
cys.cri	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
hyd.lep	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
lep.wed	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
mir.leo	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
eri.bar	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
mon.sch	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
hela.mal	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
sel.thi	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
aill.ful	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
fel	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
can	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
tal	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
gla.sab	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
gla.vol	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
hyl.pha	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
pet.set	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
bel.pea	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
pte.mom	TACCATGAGGACAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
gila.demi	TTCCCATGAGGCCAAATATCATTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60

pero.pot	TCCCCATGAGGACAAATATCATTCTGAGGTGCCACAGTAATCACAAACCTCCTATCACCAA	60
gala.mat	TCCCCATGAGGACAAATATCATTCTGAGGCCTACCGTAATCACAAACCTCCTCTCAGCAA	60
gala.moh	TTCCGTGAGGACAAATATCATTCTGAGGCCTACCGTAATCACTAACCTCCTCTCAGCAA	60
oto.gar	TCCCCATGAGGACAAATGTCACTCTGAGGCCTACCGTAATCACAAACCTCCTCTCAGCAA	60
lor.tar	TCCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACCAACCTACTATCAGCAA	60
nyc.cou	TCCCCATGAGGACAAATATCATTCTGAGGTGCCACCGTCACTCACTAACCTACTATCGGCAA	60
mus	TTCCCATGAGGACAAATATCATTCTGAGGTGCCACAGTTATTACAAACCTCCTATCAGCAA	60
gorr	TCCCCATGAGGCCAAATATCCTCTGAGGAGCCACAGTAATCACAAACTTGCTATCCGCCA	60
homo	TCCCCGTGAGGCCAAATATCATTCTGAGGGGCCACAGTAATTACAAACTTACTATCCGCCA	60
dug.dug	TCCCCATGAGGACAAATATCATTCTGAGGAGCAACCGTATTACTAACCTCCTCTCAGCTA	60
ele.max	TTCCCATGAGGACAAATATCATTCTGAGGGCAACCGTAATTACTAACCTCCTCTCAGCAA	60
afr.con	TCCCCATGAGGCCAAATATCATTCTGAGGGCAACTGTCACTCACAAACCTATACTCAGCAA	60
pavo.mut	TCCCCATGAGGTCAAATGTCACTCTGAGGGGCAACTGTTATCACAAATCTATTCTCAGCAA	60
tra.bly	TCCCCATGAGGACAAATATCATTGAGGGGCTACCGTCACTCACAAACTTATTCTCAGCAA	60
tra.sat	TCCCCATGAGGACAAATATCATTGAGGGGCTACCGTCACTCACAAATTATTCTCAGCAA	60
tra.cob	TCCCCATGAGGACAAATATCATTGAGGGGCTACCGTCACTCACAAATTATTCTCAGCAA	60
tra.tem	TCCCCATGAGGACAAATATCATTGAGGGGCTACCGTCACTCACAAATTATTCTCAGCAA	60
arg.arg	TCCCCATGAGGACAAATATCATTGAGGGGCTACTGTCACTCACAAATCTATTCTCAGCAA	60
cat.wal	TTCCCATGGGGACAAATATCATTGAGGGGCTACTGTCACTCACAAATCTATTCTCAGCAA	60
cro.cro	TCCCCATGAGGACAAATATCATTGAGGGGCTACCGTCACTCACAAATCTATTCTCAGCAA	60
sym.ree	TCCCCATGAGGACAAATATCATTGAGGGGCAACCGTCACTCACAAATTATTCTCAGCAA	60
bam.tho	TCCCCATGGGGCAAATATCCTTCTGAGGGGCTACCGTCACTCACAAATTATTCTCAGCAA	60
fra.fra	TCCCCATGAGGCCAAATATCATTCTGAGGGGCTACCGTCACTCACAAACCTATTCTCAGCAA	60
ith.cru	TACCATGAGGACAAATATCATTCTGAGGAGCCACTGTAAATCACAAACCTACTCTCAGCAA	60
ant.par	TACCATGAGGACAAATGTCACTTGGAGGGGCTACAGTCATCACCAATTCTTCTCAGCCG	60
ant.vir	TACCATGGGGACAAATGTCACTTGGAGGGGCTACAGTTATCACCAATTCTTCTCAGCCG	60
gru.ant.ant	TACCATGAGGACAAATATCATTGAGGGGCTACAGTCATCACCAATTCTTCTCAGCCG	60
gru.ant.gil	TACCATGAGGACAAATATCATTGAGGGGCTACAGTCATCACCAATTCTTCTCAGCCG	60
gru.ant.sha	TACCATGAGGACAAATATCATTGAGGGGCTACAGTCATCACCAATTCTTCTCAGCCG	60
gru.leu	TACCATGAGGACAAATATCATTGAGGGGCTACAGTCATCACCAATTCTTCTCAGCCG	60
gru.can.pra	TGCCATGAGGACAAATATCATTCTGAGGGGCTACAGTCATTACCAACCTCTTCTCAGCCG	60
gru.can.row	TGCCATGAGGACAAATATCATTCTGAGGGGCTACAGTCATTACCAACCTCTTCTCAGCCG	60
gru.can.tab	TACCATGGGGACAAATATCATTGAGGGGCTACAGTCATTACCAACCTCTTCTCAGCCG	60
gru.can.can	TACCATGGGGACAAATATCATTGAGGGGCTACAGTTATCACCAATTCTTCTCAGCCG	60
gru.ame	TACCATGGGGACAAATGTCACTTGGGGGCTACAGTTATCACCAATTCTTCTCAGCCG	60
gru.gru	TACCATGGGGACAAATATCATTGAGGGGCTACAGTTATCACCAACCTCTTCTCAGCCG	60
gru.mon	TACCATGGGGACAAATATCATTGAGGGGCTACAGTTATCACCAACCTCTTCTCAGCCG	60
gru.nig	TACCATGGGGACAAATATCATTGAGGGGCTACAGTTATCACCAACCTCTTCTCAGCCG	60
gru.jap	TACCATGGGGACAAATATCCTTCTGAGGGGCTACAGTTATCACCAACCTTCTCAGCCG	60
cic.boy	TGCCATGAGGACAGATATCATTCTGAGGGGCTACAGTCATCACCAACCTATTCTCAGCTA	60
rhe.ame	TACCATGAGGACAAATATCATTCTGAGGGGCTACAGTTATTACCAACCTATTCTCAGCCA	60
ant.alb	TACCATGAGGCCAAATATCATTCTGAGGCCTACCCCTCATCACCAACCTATTCTCAGCCA	60
fal.fam	TACCTCTGAGGACAAATATCATTCTGAGGGGCTACAGTTATCACCAACCTATTCTCAGCAA	60
fal.ver	TACCTCTGAGGACAAATATCATTCTGGGGAGCCACAGTCATCACCAACCTATTCTCAGCAA	60
fal.per	TACCTCTGAGGACAAATGTCACTCTGAGGAGCCACAGTCATTACCAACCTATTCTCAGCAA	60
fal.spa	TACCATGAGGACAAATATCATTCTGAGGAGCCACAGTCATTACCAACCTATTCTCAGCAA	60
ayt.ame	TACCATGAGGACAAATATCATTCTGAGGGGCCACCGCTGATCACCAACCTTCTCAGCCC	60
smi.sha	TCCCCATGAGGCCAAATATCATTCTGAGGGGCTACGCTTAATCACCAACCTTCTCAGCTA	60
vid.cha	TGCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATCACCAACCTATTCTCAGCAA	60
chry.pic	TACCATGGGGCAAATATCCTCTGAGGTGCCACCGTTATTACTAACCTCTCTCAGCCG	60
emy.orb.kur	TACCATGGGGCAAATATCCTCTGAGGTGCCACCGTTATTACTAACCTCTCTCAGCCG	60
che.mud	TACCATGAGGACAAATATCATTGAGGGGCCACCGTCACTCACCAACCTACTCTCAGCCG	60
eum.egr	TCCCCATGGGACAGATATCCTCTGAGGGSCAACTTAATTACCAACCTATTCTCAGCAA	60
	*** * *** * *** * *** * *** * *** * *** * *** * *** * *** * ***	
sep.mel	TCCCCATACATGCTACAAACCTACTAGAAATGTCACTGAGGAGCTTCTCACTAGACAAAAG	120
pre.ore	TTCCCATATATTGGGACAAACCTTGTAGAAATTCTGAGGAAGGATTCTCTCTCAGCAAAG	120
add.ras	TCCCCATATATCGGCACAGTTCTGCAATTAAATTCTGAGGATTCTCTCTCAGCAAAG	120

ory.dam	TCCCCATACATCGGCACAAAATTCTAGTCGAATGAAATTGAGGGGGATTCTCCGTAGACAAAG	120
hip.equ	TCCCCATATAATTGGCACAAAACCTACTGCAATGAAATCTGACGGGGATTCTCCGTAGACAAAG	120
alc.bus	TCCCCATATAATTGGCACAGACCTAGTAGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
sig.lic	TCCCCATATAATTGGCACAGACCTAGTAGAATGAAATCTGAGGAGGATTCTCACTAGACAAAG	120
bea.hun	TTCCCATATAATTGGTACAAAACCTACTGCAATGAAATCTGAGGAGCCTTCTCACTAGACAAAG	120
dam.lun	TTCCCATACATCGGCACAAAATTCTAGTCGAATGGATCTGAGGGGGCTTCTCACTAGACAAAG	120
con.tau	TCCCCATACATTGGCACTAACCTACTGCAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
amm.les	TCCCCATACATTGGCACAGACCTGOTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
pse.nay	TCCCCATATAATTGGCACAAAACCTACTGCAATGGATCTGAGGGGGATTCTCACTAGACAAAG	120
cap.ibe	TCCCCATATAATTGGCACAAAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGACAAAG	120
hem.jem	TTCCCATATAATTGGCACAAAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGATAAAAG	120
cap.fal	TCCCCATATAATTGGCACAAAACCTACTGCAATGAAATCTGAGGGGGATTCTCCGTAGACAAAG	120
rup.pyr	TCCCCATACATTGGCATAGACTTAGTCGAGTGAATCTGAGGGGGCTTCTCGGTAGACAAAG	120
rup.rup	TCCCCGTATAATTGGCACAGACCTAGTCGAATGAAATCTGAGGAGGCTTCTCGGTAGACAAAG	120
nem.cau	TCCCCATATAATTGGCACAAAACCTACTGCAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
bud.tax.tax	TCCCCATACATTGGCACAGACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
pan.hod	TCCCCATACATTGGCACAAAACCTACTGCAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
ovi.amm	TTCCCATATAATTGGCACAAAACCTACTGCAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
ovi.vig	TTCCCATATAATTGGCACAAAACCTACTGCAATGAAATCTGAGGAGGATTCTCCGTAGACAAAG	120
cap.cri	TCCCCATATAATTGGCACACAAACTTAGTAGAATGAAATCTGAGGAGGATTCTCCGTAGACAAAG	120
cvi.mos	TCCCCATACATCGGCACAAAACCTACTGCAATGAAATCTGAGGAGGATTCTCCGTAGACAAAG	120
ore.ame	TTCCCATACATCGGTACAGACCTAGTCGAATGAAATCTGAGGGGGCTTCTCACTAGACAAAG	120
cep.dor	TCCCCATACATTGGTACAAAACCTACTGCAATGAAATCTGAGGAGGCTTCTCACTAGACAAAG	120
cep.max	TCCCCATATAATTGGCACAAAACCTACTGAGTGAATCTGAGGGGGCTTCTCACTAGACAAAG	120
bis.bca	TCCCCATACATCGGCACAAAATTCTAGTCGAATGAAATCTGAGGCGGATTCTCACTAGACAAAG	120
bos.gru	TTCCCATACATCGGCACAAAATTCTAGTCGAATGAAATCTGAGGCGGTTCTCACTAGACAAAG	120
bos.tra	TCCCCATACATCGGCACAAAACCTACTGAGTGAATCTGAGGGGGATTCTCACTAGACAAAG	120
bub.min	TCCCCATACATCGGTACAAAGTCTGGTTGAATGAAATTGAGGGGGATTCTCACTAGACAAAG	120
buba.bub	TCCCCATATAATTGGCACCAACCTAGTTGAATGAAATCTGAGGAGGCTTCTCGGTAGACAAAG	120
tra.ang	TCCCCATATAATTGGCACCAACCTAGTTGAATGAAATCTGAGGAGGCTTCTCACTAGACAAAG	120
tra.eur	TTCCCATACATTGGCACAAAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGATAAGG	120
kob.ell	TCCCCATATAATTGGCACAAAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGACAAAG	120
kob.meg	TCCCCATATAATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGACAAAG	120
red.aru	TCCCCATACATCGGCACAAAACCTACTGCAATGAAATCTGAGGAGGATTCTCGATAAAAG	120
red.ful	TCCCCATACATCGGCACAAAACCTACTGCAATGAAATCTGAGGAGGATTCTCGATAAAAG	120
neo.mos	TCCCCATATAATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGACAAAG	120
pel.cap	TCCCCATACATTGGTACAAAACCTACTGCAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
gaz.dam	TCCCCATACATTGGTACAAAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGACAAAG	120
our.out	TTCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGACAAAG	120
ant.cer	TCCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGACAAAG	120
sai.tac	TCCCCATATAATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGACAAAG	120
mad.kir	TCCCCATATAATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGACAAAG	120
rap.mel	TTCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGACAAAG	120
gaz.gaz	TCCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGACAAAG	120
ant.ame	TCCCCATACATTGGTACTAACCTACTGCAATGAAATCTGAGGAGGATTCTCACTAGACAAAG	120
hyd.ina	TTCCCATACCTCGTACAAAATTCTAGTCGAATGAAATCTGAGGAGGCTTCTCACTAGATAAGG	120
mun.mun	TTCCCATATAATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGCTTCTCACTAGATAAGG	120
alc.alc	TTCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGCTTCTCACTAGACAAAG	120
cer.elia.kan	TTCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGCTTCTCACTAGACAAAG	120
cer.elia.kin	TTCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGCTTCTCACTAGACAAAG	120
cer.elia.cin	TTCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGCTTCTCACTAGACAAAG	120
cer.nip.cent	TTCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGCTTCTCACTAGACAAAG	120
cer.nip.yes	TTCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGCTTCTCACTAGACAAAG	120
cer.nip.ker	TTCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGCTTCTCACTAGACAAAG	120
cer.nip.pul	TTCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGCTTCTCACTAGACAAAG	120
cer.nip.nip	TTCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGCTTCTCACTAGACAAAG	120
cer.elia.sco	TTCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGCTTCTCACTAGACAAAG	120
cer.elia.mn	TTCCCATACATTGGCACACAAACCTACTGCAATGAAATCTGAGGAGGCTTCTCACTAGACAAAG	120

ran.car	TTCCATATAATTGGTACAAATCTAGTCGAATTGAGGAGGATTTCTGTAGATAAAG	120
mos.fus	TTCCATACATTGGTACTAAATCTGGTTGAATGAATTGAGGAGGCTTCTCACTAGACAAAG	120
mos.leu	TTCCATACATTGGTACTAAATCTGGTTGAATGAATTGAGGAGGCTTCTCACTAGACAAAG	120
mos.chr	TTCCATACATTGGTACTAAATCTGGTTGAATGAATTGAGGAGGCTTCTCACTAGACAAAG	120
mos.ber	TTCCCTACATTGGTACTAAATCTGGTTGAATGAATCTGAGGGAGGCTTCTCACTAGACAAAG	120
mos.mos	TTCCATACATTGGTACACTACCTGGTTGAAGTGAATTGAGGAGGCTTCTCACTAGACAAAG	120
tra.jav	TCCCATAATCGGCACCGAACCTAGTTGAATGAATCTGAGGCCGGTTCTCACTAGACAAAG	120
traj.nap	TCCCATAATATTGGTACTACCTTAGTCGAATGAATCTGAGGTGGCTTCTCTGTAGACAAAG	120
bala.acu	TCCCATAACATTGGTACCCCTAGTTGAATGAATCTGAGGTGGCTTCTCTGTAGACAAAG	120
bala.bcn	TCCCATAACATTGGTACTACCTTAGTCGAATGGATCTGAGGCCGGTTCTCTGTAGATAAAG	120
bala.bor	TCCCATAACATTGGTACTACCTTAGTCGAATGAATCTGGGGCGTTCTCTGTAGATAAAG	120
bala.edi	TCCCATAACATTGGTACTACCTTAGTCGAATGGGTCTGAGGCCGGTTTCTGTAGATAAAG	120
esch.rob	TCCCATAACATTGGTACTACCTTAGTCGAATGAATCTGAGGCCGGTTTCTGTGGATAAAG	120
bala.mus	TCCCATAACATTGGTACTACCTTAGTCGAATGAATCTGGGGCGTTTCTCTGTAGACAAAG	120
mega.nov	TCCCATAACATTGGTACCCCTAGTCGAATGAATCTGAGGCCGGTTCTCTGTAGATAAAG	120
bala.phy	TCCCATAACATTGGTACCCCTAGTCGAATGAATCTGAGGCCGGTTCTCTGTAGACAAAG	120
cap.mar	TCCCATAATATTGGTACCCCTAGTCGAATGAATCTGGGGCGTTTCTGTAGACAAAG	120
ceph.com	TCCCCTACATCGGTACTACCTTAGTGAATGAATCTGAGGCCGGATTTCCTGTAGACAAAG	120
ceph.eut	TCCCCTACATCGGTACTACCTTAGTGAATGAATCTGAGGCCGGATTTCCTGTAGACAAAG	120
lage.obl	TCCCCTACATCGGTACTACCTTAGTGAATGAATCTGAGGCCGGATTTCCTGTAGACAAAG	120
ceph.hea	TCCCCTACATCGGTACTACCTTAGTGAATGAATCTGAGGCCGGATTTCCTGTAGACAAAG	120
ceph.hec	TCCCCTACATCGGTACTACCTTAGTGAATGAATCTGAGGCCGGATTTCCTGTAGACAAAG	120
lage.aus	TCCCCTACATCGGTACTACCTTAGTGAATGAATCTGAGGCCGGATTTCCTGTAGACAAAG	120
lage.cru	TCCCCTACATCGGTACTACCTTAGTGAATGAATCTGAGGCCGGATTTCCTGTAGACAAAG	120
lage.obs	TCCCCTACATCGGTACTACCTTAGTGAATGAATCTGAGGCCGGATTTCCTGTAGACAAAG	120
lisso.bor	TCCCCTACATCGGCACCCCTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
lisso.per	TCCCCTACATCGGCACCCCTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
glo.mac	TCCCCTACATCGGCACCTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
glo.mel	TCCCCTACATCGGCACCTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
fere.att	TCCCCTACATCGGAACCCCTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
pepo.ele	TCCCCTACATCGGTACTACCTTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
gram.gri	TCCCCTACATCGGTACCCATTAGTGAATGAATCTGAGGCCGGATTTCCTGTAGACAAAG	120
pse.cra	TCCCCTACATCGGCACCTAGTGAATGAATCTGAGGCCGGATTTCCTGTAGACAAAG	120
lage.acu	TCCCCTACATCGGCACCCCTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
crcl.bre	TCCCCTACATCGGCACCCCTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
orca.bre	TCCCCTATATTGGCACTACCTTAGTCGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
del.cap	TCCCCTATATTGGCACTACCTTAGTCGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
del.tro	TCCCCTATATTGGCACTACCTTAGTCGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
del.del	TCCCCTATATTGGCACTACCTTAGTCGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
sten.cly	TCCCCTATATTGGCACTACCTTAGTCGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
sten.coe	TCCCCTATATTGGCACTACCTTAGTCGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
tur.adu	TCCCCTATATTGGCACTACCTTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
sten.fro	TCCCCTATATTGGCACTACCTTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
saus.chi	TCCCCTATATTGGCACTACCTTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
sten.lon	TCCCCTATATTGGCACTACCTTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
turs.tru	TCCCCTATATTGGCACTACCTTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
lage.alb	TCCCCTATATTGGCACTACCTTAGTGAATGAATCTGAGGTGGATTTCCTGTAGACAAAG	120
sten.bre	TCCCCTACATCGGCACCTAGTGAATGAATCTGAGGCCGGATTTCCTGTAGACAAAG	120
sota.flu	TCCCCTACATCGGCACCTAGTGAATGAATCTGAGGCCGGATTTCCTGTAGACAAAG	120
del.leu	TCCCCTACATCGGCACCCCTAGTGAATGAATCTGAGGCCGGTTTCCTGTAGACAAAG	120
mono.mon	TCCCCTATATTGGCACTACCTTAGTGAATGAATCTGAGGCCGGTTTCCTGTAGACAAAG	120
plat.gan	TCCCCTATATTGGCACTACCTTAGTGAATGAATCTGAGGCCGGTTTCCTGTAGACAAAG	120
plat.min	TCCCCTATATTGGCACTACCTTAGTGAATGAATCTGAGGCCGGTTTCCTGTAGACAAAG	120
kogi.bre	TCCCCTACATCGGCACCCCTAGTGAATGAATCTGAGGCCGGTTTCCTGTAGACAAAG	120
kogi.sim	TCCCCTACATCGGCACCCCTAGTGAATGAATCTGAGGCCGGTTTCCTGTAGACAAAG	120
phys.cui	TCCCCTATATTGGCACTACCTTAGTGAATGAATCTGAGGCCGGTTTCCTGTAGACAAAG	120
lipo.vek	TCCCCTACATCGGCACCCCTAGTGAATGAATCTGAGGCCGGTTTCCTGTAGACAAAG	120
phoc.sin	TCCCCTACATCGGCACCTAGTGAATGAATCTGAGGCCGGTTTCCTGTAGACAAAG	120

bera.bai	TTCCCTTATATCGCACCACACTCTTCGAATGAAATCTGAGGTGGCTTCTCCGTAGATAAAG	120
ziph.car	TCCCCCTATATCGGCACACTACTCTAGTCGAATGAAATCTGAGGTGGTTTTCTAGTAGATAAAG	120
meso.eur	TCCCCCTATATTGGCACTACTCTAGTCGAATGAAATCTGAGGTGGCTTTCTCCGTAGATAAAG	120
meso.bid	TTCCCTACATCGGCACCTACCCCTAGTCGAATGAAATCTGAGGTGGCTTTCTCCGTAGACAAG	120
meso.den	TTCCCTATATTGGCACCCACCTAGTCGAATGAAATCTGAGGTGGCTTTCTCCGTAGACAAG	120
hype.amp	TTCCCTATATCGGCACCTACCCCTAGTCGAATGAAATCTGAGGTGGCTTTCTCCGTAGATAAAG	120
meso.per	TCCCCCTATATTGGCACCCACCTAGTCGAATGAAATTCTAGGTGGCTTCTCCGTAGACAAG	120
ponc.bla	TCCCCCTACATCGGCACCTACCCCTAGTCGAATGAAATCTGAGGTGGCTTTCTCCGTAGACAAG	120
hex.lib	TCCCCCTACATGGAACAGACACCTAGTCGAATGAAATCTGAGGTGGCTTCTCCGTAGATAAAG	120
hipp.amp	TCCCCCTATATTGGAACAGACACCTAGTCGAATGAAATCTGAGGTGGCTTCTCCGTAGACAAG	120
dic.sum	TCCCCATACATCGGCACCCGACCTTCTAGAAATGAAATCTGAGGGGGATTCTCCGTAGACAAG	120
rhin.son	TCCCCCTATATCGGTACCAACCTTCTAGAGTCGAATCTGAGGAGGATTCTCGACACAAG	120
cera	TCCCCATACATCGGCACCAACCTCGTAGAAATGAAATCTGAGGAGGATTCTCGACACAAG	120
equu	TCCCCCTACATCGGTACCTACGGTCGTGAAATGAAATCTGAGGTGGATTCTCGACACAAG	120
baby.bab	TCCCCCTATATCGGAACGGACCTCGTAGAAATGAAATCTGAGGAGGCTTCTCCGTAGATAAAG	120
phac.afr	TCCCCCTATATCGGAACAGACCTCGTAGAAATGAAATCTGAGGGGGCTTCTCGACACAAG	120
sus.bar	TCCCCCTATATCGGAACAGACCTCGTAGAAATGAAATCTGAGGGGGCTTCTCGACACAAG	120
sus.scr.ewb3	TCCCCCTATATCGGAACAGACCTCGTAGAAATGAAATCTGAGGGGGCTTCTCGACACAAG	120
lama.gla	TCCCCATATCGGAACAAACCTTCTAGAAATGAAATCTGAGGGGGTTCTCCGTGACACAAG	120
lama.gua	TCCCCATATCGGAACAAACCTTCTAGAAATGAAATCTGAGGGGGCTTCTCGACACAAG	120
vic.vic	TCCCCCTATATCGGAACAAACCTTCTAGAAATGAAATCTGAGGGGGCTTCTCGACACAAG	120
cam.bac	TCCCCCTATATCGGAACAAACCTTCTAGAAATGAAATCTGAGGGGGCTTCTCGACACAAG	120
arc.for	TCCCCCTACATGGGACCAACCTAGTCGAATGAAATTCTAGGTGGATTCTCGACACAAG	120
arc.gaz	TCCCCCTACATGGGACCAACCTAGTCGAATGAAATTCTAGGTGGATTCTCGACACAAG	120
eum.jub	TCCCCCTACATGGGACCAACCTAGTCGAATGAAATTCTAGGTGGATTCTCGACACAAG	120
sal.cal	TCCCCCTACATGGGACCAACCTAGTCGAATGAAATTCTAGGTGGATTCTCGACACAAG	120
odo.zos	TCCCCCTATGTAGGGACTGACTGGTCGAATGAGTCGAGGTGGGGTTCTCGACACAAG	120
pho.fasciata	TCCCCCTATATCGGAACCGACCTAGTCGAATGAAATCTGAGGAGGATTCTCGACACAAG	120
pho.gro	TCCCCCTACATCGGAACCGATCTAGTCGAATGAAATCTGAGGAGGTTCTCGACACAAG	120
pho.vit	TCCCCCTATATCGGAACCGATCTAGTCGAATGAAATCTGAGGAGGTTCTCGACACAAG	120
cys.cri	TCCCCCTACATCGGAACCGATCTAGTCGAATGAAATTCTAGGTGGGGATTCTCGACACAAG	120
hyd.lep	TCCCCCTACATCGGAACCGACCTAGTCGAATGAAATTCTAGGTGGGGATTCTCGACACAAG	120
lep.wed	TCCCCCTACATCGGAACCTAGTCGAATGAAATTCTAGGTGGGGATTCTCGACACAAG	120
mir.leo	TCCCCCTATGTGGAGACGACCTAGTCGAATGAAATTCTGAGGAGGATTCTCGACACAAG	120
eri.bar	TCCCCCTACATCGGAACCGATCTAGTCGAATGAAATTCTGAGGAGGATTCTCGACACAAG	120
mon.sch	TCCCCCTATATCGGAACCGATCTAGTCGAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
hela.mal	TCCCCCTATATTGGAACCGACCTAGTCGAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
sel.thi	TCCCCCTATATTGGAACCGACCTAGTCGAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
ail.ful	TCCCCCTATATTGGAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
fel	TTCCCATACATCGGAACCTAGTCGAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
can	TCCCCCTATATCGGAACCTAGTCGAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
tal	TCCCCCTACATCGGTACAGACACTAGTCGAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
gla.sab	TCCCCCTATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
gla.vol	TTCCCCCTATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
hyl.pha	TCCCCCTACATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
pet.set	TCCCCCTATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
bel.pea	TCCCCCTATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
pse.mcm	TCCCCCTATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
gala.demi	TCCCCCTATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
pero.pot	TCCCCCTATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
gala.mat	TCCCCCTACATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
gala.moh	TCCCCCTACATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
cto.gar	TCCCCCTACATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
lot.tas	TCCCCCTACATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
nyc.con	TCCCCCTACATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
mus	TCCCCCTACATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
zecc	TCCCCCTACATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120
homo	TCCCCCTACATATTGGACCAACCTTGAGACTGAAATGAAATTCTGAGGAGGCTTCTCGACACAAG	120

dug.dug	TCCCCTACATCGGCACCAACCTAGTCGAATGAGTTGAGGGGGATTCTCAGTAGACAAAG	120
ele.max	TTCCCTACATCGGCACAAACCTAGTAGAATGAATTGAGGAGGCTTTTGGTAGATAAACG	120
afr.con	TCCCCTATATTGGCAAAACCTAGTAGAATGGGCCTGAGCAGGGATTCTCAGTTGACAACC	120
pavo.mut	TCCCTTATATTGGACAAAACCTAGTAGAATGACCCCTGAGGGGGATTCTCAGTTGACAACC	120
tra.bly	TCCCATACTTGGCAAAACCTAGTAGAATGAGCCTGAGGAGGCTTTTCAAGTTGACAATC	120
tra.sat	TCCCATACTTGGCAAAACCTAGTAGAATGAGCCTGAGGGGGCTTTTCAAGTTGACAATC	120
tra.cob	TCCCATACTTGGCAAAACCTAGTAGAATGAGCCTGAGGGGGCTTTTCAAGTTGACAATC	120
tra.tem	TCCCATACTTGGCAAAACCTAGTAGAATGAGCCTGAGGGGGCTTTTCAAGTTGACAATC	120
arg.arg	TCCCTTATATTGGACAAAACCTAGTAGAATGAGCCTGAGGAGGATTCTCAGTTGACAATC	120
cat.wal	TCCCTTACATCGGACAGACCTAGTAGAATGAGCCTGAGGAGGATTCTCAGTTGACAACC	120
cro.cro	TCCCTTACATGGCAAAACCTAGTCAGTGAGCTGACGGGGATTCTCAGTTGACAACC	120
sym.ree	TCCCCTACATCGGACAAACCTAGTAGAATGAGCCTGAGGAGGATTCTCAGTTGACAACC	120
bam.tho	TTCCCTACATCGGACAAACCTAGTAGAATGAGCCTGGGGGGATTCTCAGTAGACAACC	120
fra.fra	TTCCCTACATGGACAAACCTAGTAGAATGAGCCTGAGGGGGATTCTCAGTAGACAACC	120
ith.cru	TTCCCTACATGGCAAAACCTGTAGAATGAGCTTGAGGAGGATTCTCAGTAGACAACC	120
ant.par	TCCCATACTGGCAAAACCTGTAGAATGAGCTTGAGGGGGTTTCTCAGTAGACAATC	120
ant.vir	TCCCATACTGGCAAAACCTGTAGAATGAGCTTGAGGGGGTTTCTCAGTAGACAATC	120
gru.ant.ant	TCCCCTACATGGCAAAACCTGTAGAATGAGCTTGAGGGGGCTTCTCAGTAGACAATC	120
gru.ant.gil	TCCCCTACGGGGCAAAACCTGTAGAATGAGCTTGAGGGGGCTTCTCAGTAGACAATC	120
gru.ant.sha	TCCCCTACATGGCAAAACCTGTAGAATGAGCTTGAGGGGGCTTCTCAGTAGACAACC	120
gru.leu	TCCCATACTGGCAAAACCTGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAATC	120
gru.can.pra	TCCCATACTGGCAAAACCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAATC	120
gru.can.row	TCCCATACTGGCAAAACCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAATC	120
gru.can.tab	TCCCATACTGGCAAAACCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAATC	120
gru.can.can	TCCCATACTGGCAAAACCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAATC	120
gru.ame	TCCCATACTGGCAAAACCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAACC	120
gru.gru	TCCCATACTGGCAAAACCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAACC	120
gru.mon	TCCCATACTGGCAAAACCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAACC	120
gru.nig	TCCCATACTGGCAAAACCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAACC	120
gru.jap	TCCCATACTGGCAAAACCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAACC	120
cic.boy	TCCCCTACATGGCAAAACCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAACC	120
the.ame	TCCCCTACATGGCAAAACCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAACC	120
ant.alb	TCCCATACTGGCAAAACCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAATC	120
fal.fam	TCCCATACTGGCAAAACCTAGTCGAATGGGCTTGAGGGAGGATTCTCAGTAGACAACC	120
fal.ver	TCCCATACTGGCAAAACCTAGTCGAATGGGCTTGAGGGAGGATTCTCAGTAGACAACC	120
fal.per	TCCCATACTGGCAAAACCTAGTCGAATGGGCTTGAGGGAGGATTCTCAGTAGACAACC	120
fal.spa	TCCCATACTGGCAAAACCTAGTCGAATGGGCTTGAGGGAGGATTCTCAGTAGACAACC	120
ayt.ame	TCCCATACTGGCAAAACCTGTAGAATGGGCTTGAGGGGGATTCTCAGTAGACAACC	120
smi.sha	TTCCATACTGGCACAAACCTAGTAGAATGGGCTTGAGGGGGATTCTCAGTAGACAACC	120
vid.cha	TTCCATACTGGCAAAACCTAGTAGAATGGGCTTGAGGGGGATTCTCAGTAGACAACC	120
chry.pic	TCCCATTCAATTGGTAACACATTAGTACAATGAATGAGCTTGAGGGGGATTCTCAGTAGACAACC	120
emy.osb.kuz	TCCCATACTGGCAAAACACTAGTCGAATGAATGAGGGGGATTCTCAGTAGACAATG	120
che.mud	TCCCATACTGGCAAAACACTAGTCGAATGAATGAGGGGGATTCTCAGTAGACAATG	120
eum.egr	TCCCATACTGGCAAAACCTAGTAGAATGAATTGAGGGGGCTTTCTCAGTAGACAATG	120
* * * * *		
aep.mel	CAACCCCTNACCCGATTTTGGTTCACCTTCATGTTGATTGATGATTGCGGCACTAG	130
ore.ore	CAACCCCTAACCGGATTTTGGCTTTCATGTTGATTGATGCGGCACTAG	130
add.nas	CAACCCCTAACCGGATTTTGGCTTTCACCTTTATTTGTTGCTTTCATGCGGCACTAG	130
cty.dam	CAACCCCTAACCGGATTTTGGCTTTCACCTTTATTTGTTGCTTTCATGCGGCACTAG	130
hip.equ	CAACCCCTAACCGGATTTTGGCTTTCACCTTTATTTGTTGCTTTCATGCGGCACTAG	130
alc.bus	CAACCCCTAACCGGATTTTGGCTTTCACCTTTATTTGTTGCTTTCATGCGGCACTAG	130
sig.lis	CAACCCCTAACCGGATTTTGGCTTTCACCTTTATTTGTTGCTTTCATGCGGCACTAG	130
bea.hun	CAACCCCTAACCGGATTTTGGCTTTCACCTTTATTTGTTGCTTTCATGCGGCACTAG	130
dam.lun	CAACCCCTAACCGGATTTTGGCTTTCACCTTTATTTGTTGCTTTCATGCGGCACTAG	130
con.tau	CAACCCCTAACCGGATTTTGGCTTTCACCTTTATTTGTTGCTTTCATGCGGCACTAG	130
num.les	CAACCCCTAACCGGATTTTGGCTTTCACCTTTATTTGTTGCTTTCATGCGGCACTAG	130
psc.may	CAACCCCTAACCGGATTTTGGCTTTCACCTTTATTTGTTGCTTTCATGCGGCACTAG	130

cap.ibe	CCACTCTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCATTACAGCCCTCG	180
hem.jem	CTACCCCTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCATTACAGCCCTCG	180
cap.fal	CCACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCATTGCAGGCCCTCG	180
rup.pyr	CTACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCATTGCAGGCCCTCG	180
rup.rup	CTACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCATTGCAGGCCCTCG	180
nem.cau	CTACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCATTACAGCTACTG	180
bud.tax.tax	CATCCCTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCATTGCAGGCCCTCG	180
pan.hod	CTACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCATTGCAGGCCCTCG	180
ovi.amm	CCACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCAGGCCCTCG	180
ovi.vig	CTACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCAGGCCCTCG	180
cap.cri	CCACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCAGGCCCTCG	180
ovi.mos	CCACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCAGGCCCTCG	180
ore.ame	CTACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCAGGCCCTCG	180
cep.dor	CAACTCTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATCAGGCCCTCG	180
cep.max	CAACCCCTACTCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATACCAATTG	180
bis.bon	CAACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATACCAATTG	180
bos.gru	CAACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATACCAATTG	180
bos.tra	CAACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATACCAATTG	180
bub.mia	CAACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATACCAATTG	180
buba.bub	CAACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATACCAATTG	180
tra.ang	CAACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATACCAATTG	180
tra.eur	CAACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATACCAATTG	180
kob.ell	CAACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATACCAATTG	180
kob.meg	CAACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATACCAATTG	180
red.aru	CAACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATACCAATTG	180
red.ful	CAACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATACCAATTG	180
neo.mos	CAACCCCTACCCGATTCTGCCTTCACTTCATCCTCCCATTCACTCATACCAATTG	180
pel.cap	CAACACTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
gaz.dam	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
our.our	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
ant.cer	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
sai.tat	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
mad.kir	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
rap.mel	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
gaz.gaz	CAACACTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
ant.ame	CAACACTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
hyd.lne	CAACACTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
mun.mun	CAACACTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
alc.alc	CAACACTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
cer.elia.kan	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
cer.elia.xan	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
cer.elia.can	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
cer.nip.cenc	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
cer.nip.yes	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
cer.nip.ker	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
cer.nip.pul	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
cer.nip.nip	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
cer.elia.scd	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
cer.dam	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
san.sar	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
mos.fus	CAACACTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
mos.leu	CAACACTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
mos.chs	CAACACTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
mos.bes	CAACACTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
ros.mos	CAACACTCACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
tra.jay	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
tra.rup	CAACCTTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180
cul.ain	CAACATTAACCGGATTCTGCCTTCACTTCATCCTCCCATTCACTCATGCAGGCCCTCG	180

bala.bon	CAACATTAAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
bala.bor	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
bala.edi	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
esch.rob	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
bala.mus	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
mega.nov	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
bala.phy	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
cap.mar	CGACACTAACCTCGCTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
ceph.com	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
ceph.euc	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
lage.obl	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
ceph.hea	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
ceph.hec	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
lage.aus	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
lage.cru	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
lage.obs	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
lisso.bor	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
lisso.per	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
glo.mac	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
glo.mel	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
fera.att	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
pepo.ele	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
gram.gri	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
pse.cra	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
lage.acu	CAACACTGACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
orci.bre	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
orca.bre	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
del.cap	CAACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
del.tro	CAACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
del.del	CAACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
sten.cly	CAACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
sten.coe	CAACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
tur.adu	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
sten.fro	CAACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
saus.chi	CAACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
sten.lon	CAACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
turs.bru	CAACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
lage.alb	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
sten.bre	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
sota.flu	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
del.leu	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
mono.mon	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
plat.gan	CAACACTAACACGATTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
plat.mia	CAACACTAACACGATTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
kogi.bre	CAACACTAACACGATTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
kogi.sim	CCACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
phys.cat	CTACGGCTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
lico.vex	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
phoc.sin	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
bera.bat	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
ciph.cat	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
meso.glo	CTACACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
meso.bld	CCACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
meso.den	CTACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
myope.imp	CTACATTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
meso.pes	CAACACTAACACGCTTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
peant.b1	TCACCTTACACCACTTTCCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTTAG 180
hex.lib	

hipp.amp	CCACCCCTAACAGGATTCTTGCCTTCACTTATTCTTCATTGCTTATCACAGCACTAG	130
dic.sum	CCACCCCTCACCCGGTTCTTGCCTTCACTTCATCCTCCCCCTTCATCATCCTAGCCCTAG	130
chin.son	CTACCCCTAACCGATTCTTGCCTTCACTTCATCCTTEGCTTATTATCCTAGCTTAG	130
cera	CCACACCTAACAGGATTCTTGCCTTCACTTATCCTCCCCCTTATTATCATAACGGCTTAG	130
equu	CCACCCCTAACCGATTCTTGCCTTCACTTATTCTACCCCTTATCATCACAGGGCTTG	130
baby.bab	CAACCCCTCACAGGATTCTTGCCTTCACTTATTCTACCCCTTATCATCATCACCCGCTCG	130
phac.afr	CAACTCTCACAGGATTCTTGCCTTCACTTCATTTACCTTTATCATCGCTGCCCTAG	130
sus.bar	CAACCCCTAACAGGATTCTTGCCTTCACTTATCCTGCCATTACATTACGGCCCTCG	130
sus.scr.ewb3	CAACCCCTCACACGATTCTTGCCTTCACTTATCCTGCCATTACATTACGGCCCTCG	130
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lama.gua	CCACCCCTAACCGATTCTTGCCTTCACTTATCCTACCTTTGTCAATTGCAGCTCTAG	130
vic.vic	CCACCCCTAACCGATTCTTGCCTTCACTTATCCTACCTTTGTCAATTGCAGCTCTAG	130
cam.bac	CCACCCCTCACACGATTCTTGCCTTCACTTATCCTGCCATTATTATCACGGCCCTAG	130
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arc.gaz	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTCCCTTCTAGCATCAGCACTAG	130
eum.jub	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTOCCCCTTCTAGCATCAGCACTAG	130
zal.cal	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTOCCCCTTCTAGCATCAGCACTAG	130
odo.ros	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTACCCATTGTAGTRTCAGCACTAG	130
pho.fasciata	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTACCCATTGTAGTRTCAGCACTAG	130
pho.gro	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTACCCATTGTAGTRTCAGCACTAG	130
pho.vit	CAACTCTAACACGGTTTCTGCCTTCACTTCATCCTACCCATTGTAGTRTCAGCACTAG	130
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hyd.lep	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTCCCTTCTAGTRTCAGCACTAG	130
lep.wed	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTCCCTTCTAGTRTCAGCACTAG	130
mir.leo	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTACCCATTGTAGTRTCAGCACTAG	130
eri.bar	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTACCCATTGTAGTRTCAGCACTAG	130
mon.sch	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTACCCATTGTAGTRTCAGCACTAG	130
hela.mal	CGACTCTAACACGATTCTTGCCTTCACTTATCCTCCGTTCATCATCTTGGCACTAA	130
sel.thi	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTCCGTTCATCATCTTGGCACTAA	130
ail.ful	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTCCGTTCATCATCTTGGCACTAA	130
fel	CAACCCCTAACACGATTCTTGCCTTCACTTATCCTCCGTTCATCATCTTGGCACTAA	130
can	CGACACTCACACGATTCTTGCCTTCACTTCATCTGCCATTATTGTGGCACTAG	130
tal	CTACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
gla.sab	CTACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
gla.vol	CTACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
hy1.pha	CTACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
pet.set	CTACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
bel.pea	CTACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
pse.mom	CTACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
gala.demi	CTACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
pero.pot	CTACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
gala.mat	CTACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
gala.moh	CTACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
oto.gac	CAACCCCTCACACGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
lor.tac	CAACCCCTCACACGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
nyc.con	CAACCCCTGACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
mus	CTACCCCTAACACGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
gorr	CTACCCCTAACACGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
homo	CGACCCCTCACACGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
dug.dug	CGACCCCTCACACGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
ele.max	CAACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
aff.con	CAACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
pavo.mut	CAACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
ica.bly	CAACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
ica.cat	CAACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
ica.zeb	CAACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
ica.bem	CAACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130
ica.ice	CAACCCCTAACCGATTCTTGCCTTCACTTATCCTCCCTTATTATTGTGCTGCCCTAG	130

cat.wal	CAACTCTACCCGATTCTCGCCCTGCACCTCTCCTCCCTCGTAATTGCAGGAATCA	130
cro.cro	CAACCCCTCACCCGATTCTCGCCCTACACTCTCTCCCTCCCTCGTAATTGCAGGAATCA	130
sym.ree	CAACCCCTCACCCGATTCTCGCCCTACACTCTCTCCCTACACCGAATCA	130
bam.cho	CAACTCTACCCGATTCTCGCCCTACACTCTCTACTCCCTCGTAATTGCAGGAATCA	130
fra.fra	CAACCCCTCACCCGATTCTCGCCCTACACTCTCTCGTAATTGCAGGAATCA	130
ith.cru	CAACCCCTCACCCGATTCTCGCCCTACACTCTCTCGTAATTGCAGGAATCA	130
anc.par	CCACATTAACTCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
anc.vit	CCACATTAACTCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
gru.ant.anc	CCACATTAACTCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
gru.ant.gil	CCACATTAACTCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
gru.ant.sha	CCACATTAACTCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
gru.leu	CCACATTAACTCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
gru.can.pra	CCACATTAACCCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
gru.can.row	CCACATTAACCCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
gru.can.tab	CCACATTAACCCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
gru.can.can	CCACATTAACCCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
gru.ame	CCACATTAACCCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
gru.gru	CCACATTAACCCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
gru.mcn	CCACATTAACTCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
gru.nig	CCACATTAACTCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
gru.jap	CCACATTAACCCGATTCTACCTTACACTCTCTCCATTCTATAATTATAGGCCTCA	130
cic.boy	CTACCTAACCCGATTCTCGCCCTGCACTCTCTCTCCATTCTATAATTAGGCCTAA	130
rhe.ame	CAACCTGACACGATTCTCGCCCTACACTCTCTCCGGTCTATAATTGCAGGCCTAG	130
ant.alb	CAACACTGACCCGATTCTCGCCCTACACTCTCTCCATTCTATAATTGCAGGGCTCA	130
fal.fam	CAACACTAACCGATTCTCGCCCTACACTCTCTCCATTCTATAATTGCAGGGCTCA	130
fal.ver	CAACACTGACCCGATTCTCGCCCTACACTCTCTCCATTCTATAATTGCAGGACTCA	130
fal.per	CAACACTAACCGTTCTCGCCCTACACTCTCTCCATTCTATAATTGCAGGGCTTA	130
fal.spa	CAACACTAACCGATTCTCGCCCTACACTCTCTCCATTCTATAATTGCAGGGCTCA	130
ayt.ame	CCACCTAACCGATTCTCGCCCTACACTCTCTCCATTCTATAATTGCAGGGCTCA	130
smi.sha	CAACACTAACCGATTCTCGCCCTACACTCTCTCCATTCTATAATTGCAGGGCTCA	130
vid.cha	CAACCTAACCGATTCTCGCCCTACACTCTCTCCATTCTATAATTGCAGGGCTAA	130
chry.pic	CAACCTAACCGATTCTCGCCCTACACTCTCTCCATTCTATAATTAGGCCTAA	130
emy.orb.kur	CAACCTAACCGATTCTCGCCCTACACTCTCTCCATTCTATAATTAGGCCTAA	130
che.mud	CAACCTAACCGATTCTCGCCCTACACTCTCTCCATTCTATAATTAGGGGCTTA	130
eum.egr	CAACCTCACCCGATTCTACATTCCACTCTCTCTGGTCTATAATTGGGCTATTATAGGGGCT	130
* * * * *		
aep.mel	CCATAGTCCACCTACTCTTCTCGAAACAGGATCTAACACCCCTACAGGAATCTCAT	240
ore.ore	CCATAGTACACCTACTCTTCTCGAAACAGGATCTAACACCCCTACAGGAATCTCAT	240
add.nas	CCATAGTCCATCTACTCTTCTCGAAACAGGATCTAACACCCCTACAGGAATCTCAT	240
ory.dam	CCATAGTCCACCTACTCTTCTCGAAACAGGATCTAACACCCCTACAGGAATCACCT	240
hip.equ	CCATAGTACACCTACTCTTCTCGATGAGACAGGATCTAACACCCCTACAGGAATTGAT	240
alc.bus	CCATAGTTCACCTCTTATTCTCGAACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	240
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bea.hun	CCATAGTCCACCTCTTATTCTCGAACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	240
dam.lun	CCATAGTCCACCTCTTATTCTCGAACGAAACAGGATCTAACACCCCTACAGGAATTTCAT	240
con.tau	CTATAGTCCATCTCTTATTCTCGAACGAAACAGGATCTAACACCCCTACAGGAATTTCAT	240
amm.les	CCATAGTCCACCTACTTTCTCGAACGAAACAGGATCTAACACCCCTACAGGAATCCAT	240
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cap.ibe	CCATAGTCCACCTACTTTCTCGAACGAAACAGGATCTAACACCCCTACAGGAATCCAT	240
hem.jem	CCATAGTCCACCTACTTTCTCGAACGAAACAGGATCTAACACCCCTACAGGAATCCAT	240
cap.fal	CCATAGTCCACCTACTTTCTCGAACGAAACAGGATCTAACACCCCTACAGGAATCCAT	240
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sup.sup	CCATAGTCCACCTACTTTCTCGAACGAAACAGGATCTAACACCCCTACAGGAATCCAT	240
nem.tan	CTATAGTCCACCTACTTTCTCGAACGAAACAGGATCTAACACCCCTACAGGAATCCAT	240
bud.tan.tan	CCATAGTCCACCTTTCTCGAACGAAACAGGATCTAACACCCCTACAGGAATCCAT	240
sun.hod	CCATAGTCCACCTTTCTCGAACGAAACAGGATCTAACACCCCTACAGGAATCCAT	240
ovi.lam	CCATAGTCCACCTTTCTCGAACGAAACAGGATCTAACACCCCTACAGGAATCCAT	240

ovi.vig	CTATAGTTCACCTACTCTTCCACGAAACAGGATCCAATAACCCCACAGGAATTCCAT	240
cap.cri	CCATAGTCACCTACTTTCTCCACGAAACAGGATCCAACAACCCCACAGGAATTCCAT	240
ovi.mos	CTATAGTACATTTGTCTTCCACGAAACAGGATCCAACAACCCCACAGGAATTCCAT	240
ore.ame	CCATAGTCCACTTACTTTCTCCACGAAACAGGATCTAATAACCCAAACAGGAATTCCAT	240
cep.dor	CCATAGTCACCTACTCTTCCATGAAACAGGATCCAACAACCCCACAGGAATTCCAT	240
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bis.ben	CCATAGTCACCTACTATTCTCCACGAAACAGGTTCTAACAATCCAACAGGAATTCCAT	240
bos.gtu	CCATAGTCCACCTACTATTCTCCACGAAACAGGCTCCAACAATCCAACAGGAATTCCAT	240
bos.tra	CAATAATCCATCTACTCTTCCATGAAACAGGGTCTAACATCCAAACAGGAATTCCAT	240
bub.min	CAATAGTCCACCTATTCTTCTCCACGAAACAGGATCCAACAACCCAAACAGGAATTCCAT	240
buba.bub	CAATAGTCCACCTATTCTTCTCCACGAAACAGGATCCAACAACCCAAACAGGAATTCCAT	240
tra.ang	TTATGGTCCACCTATTCTTCTCCATGAAACAGGATCCAACAACCCAAACAGGAATTCCAT	240
tra.eur	CCATGGTACACCTACTATTCTCCACGAAACAGGATCCAACAACCCAAACAGGRATCCAT	240
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red.ful	CTATAGTCCACCTACTATTCTCCATGAAACAGGATCCAACAACCCAAACAGGAATTCCAT	240
neo.mos	CCATAGTCCACTTACTCTTCCACGAAACAGGATCCAACAACCCAAACGGGAATTCCAT	240
pel.cap	CCATAGTACACTTGTTTTCTCATGAAACAGGATCTAACAAACCCAAACAGGAATTCCAT	240
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our.our	CCACAGTCCACCTACTTTCTTACGAAACAGGGATCCAACAATCCCACAGGAATTCCAT	240
ant.cer	CCATAGTACACCTACTGTTTCTTACGAAACAGGATCCAACAACCCAAACAGGAATTCCAT	240
sai.tat	CTATAGTCCACCTACTTTTCTTACGAAACAGGATCTAACAAACCCAAACAGGAATTCCAT	240
mad.kir	CCATGGTCACTCTCTTCTCCATGAAACGGGATCCAACAACCCAAACAGGAATTCCAT	240
rap.mel	CTATAGTCACCTACTTTCTCCACGAAACTGGATCCAACAACCCAAACAGGAATTCCAT	240
gaz.gaz	CTATAGTCCACTTATTATTCTTCTCCATGAAACAGGATCCAATAACCCACAGGAATTCCAT	240
anz.ame	CCATAGTACACTTACTATTCTCCACGAAACAGGATCCAACAACCCAAACAGGAATTCCAT	240
hyd.ine	CCATAGTGCACCTACTTTCTCCACGAAACAGGATCCAACAACCCAAACAGGAATTCCAT	240
mun.mun	CTATAGTCCACCTACTTTCTCCACGAAACAGGATCCAACAACCCAAACAGGAATTCCAT	240
alc.alc	CCATAGTCCACCTACTTTCTTACGAAACAGGATCCAACAACCCAAACAGGAATTCCAT	240
cer.el.a.kan	CTATAGTACACTTACTCTTCTTACGAAACAGGATCCAATAACCCAAACAGGAATTCCAT	240
cer.el.a.xan	CTATAGTACACTTACTCTTCTTACGAGACAGGATCTAACCCAAACAGGAATTCCAT	240
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cer.nip.nip	CTATAGTACACTTACTCTTCTTACGAAACAGGATCTAACCCAAACAGGAATTCCAT	240
cer.el.a.sco	CTATAGTACACTTACTCTTCTTACGAAACAGGATCTAACCCAAACAGGAATTCCAT	240
cer.dam	CTATAGTACATTACTCTTCTTACGAGACAGGATCCAATAACCCAAACAGGAATTCCAT	240
ran.tar	CTATAGTCCATTGCTTCTTACGAAACAGGGTCTAACAAACAGGAATTCCAT	240
mos.fus	CTATGGTCACTACTCTTCTCCACGAAACAGGATCCAACAACCCAAACAGGAATTCCAT	240
mos.leu	CTATGGTCACTACTCTTCTCCACGAAACAGGATCCAACAACCCAAACAGGAATTCCAT	240
mos.chz	CTATGGTCACTACTCTTCTCCACGAAACAGGATCCAACAACCCAAACAGGAATTCCAT	240
mos.bez	CCATGGTCACTACTCTTCTCCACGAAACAGGATCCAACAACCCAAACAGGAATTCCAT	240
mos.mos	TCCTAGTCCACCTTATTCTTACGAAACAGGATCTAACCCCCACAGGAATTCCAT	240
tri.jav	CCCTAGTCCACCTTATTCTTACGAGACAGGATCAAATAACCCAAACAGGAATTCCAT	240
trig.cap	CAATTGTCACCTTATTCTTACGAAACAGGATCAAATAACCCAAACAGGAATTCCAT	240
bala.atu	CAATTGTCACCTTATTCTTACGAAACAGGATCAAATAACCCAAACAGGAATTCCAT	240
bala.bon	CAATTGTCACCTTATTCTTACGAAACAGGATCAAATAACCCAAACAGGAATTCCAT	240
bala.boc	CAATTGTCACCTTATTCTTACGAAACAGGATCAAATAACCCAAACAGGAATTCCAT	240
bala.edi	CAATTGTCACCTTATTCTTACGAAACAGGATCAAATAACCCAAACAGGAATTCCAT	240
esch.spo	CAATTGTCACCTTATTCTTACGAAACAGGATCAAATAACCCAAACAGGAATTCCAT	240
bill.mus	CAATTGTCACCTTATTCTTACGAAACAGGATCAAATAACCCAAACAGGAATTCCAT	240
meg.oow	CAATTGTCACCTTATTCTTACGAAACAGGATCAAATAACCCAAACAGGAATTCCAT	240
bala.phy	CAATTGTCACCTTATTCTTACGAAACAGGATCAAATAACCCAAACAGGAATTCCAT	240
cap.muc	CAATTGTCACCTTATTCTTACGAAACAGGATCAAATAACCCAAACAGGAATTCCAT	240
deph.com	CAATTGTCACCTTATTCTTACGAAACAGGATCAAATAACCCAAACAGGAATTCCAT	240

ceph.eut	CAGCCGTCCACCTACTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
lage.obl	CAGCCGTCCACCTACTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
ceph.hea	CAGCCGTCCATCTACTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
ceph.hec	CAGCCGTCCACCTACTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
lage.aus	CAGCCGTCCACTTACTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
lage.cru	CAGCCGTCCACCTGCTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
lage.obs	CAGCCGTCCACCTACTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
lisso.bor	CAGCTGTTCACCTACTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
lisso.per	CAGCTGTTCACCTACTGTTCTACACGAGACAGGATCCAATAACCCCACAGGAATCCCAT	240
glo.mac	TAGCTGTCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCATAAGGAATCCCAT	240
glo.mel	TAGCTGTTCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
fere.att	TAGCTGTCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
pepo.ele	TAGCTGTTCACCTGCTATTCTACACGAGACAGGATCCAATAACCCCACAGGAATCCCAT	240
gram.gri	CAGCTACCCACCTACTATTCTACACGGAGACTGGATCCAATAACCCCACAGGAATCCCAT	240
pse.cra	CAGCTGTTCACCTGCTTCTACACGAGACAGGATCCAATAACCCACAGGAATCCCAT	240
lage.acu	CAGCTGTTCACCTACTGTTCTACACGAGACAGGATCCAATAACCCCACAGGAATCCCAT	240
orci.bre	CAGCTGTTCACCTACTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
orca.bre	TAACCTGTTCACCTACTATTCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
del.cap	CAGCCGTTCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
del.tro	CAGCCGTTCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
del.del	CAGCCGTTCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
sten.cly	CAGCCGTTCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
sten.coe	CAGCCGTTCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
tur.adu	CAGCCGTTCACCTACTATTCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
sten.fro	CAGCCGTTCACCTACTATTCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
saus.chi	TAGCCGTTCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
sten.lon	CAGCCGTTCACCTACTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
turs.tru	CAGCCGTTCACCTACTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
lage.alb	TAGCTGTCACCTACTATTCTACACGAGACAGGATCCAACAACCCCACAGGAATCCCAT	240
sten.bre	CAACTGTCACCTACTATTCTACACGAGACAGGATCCAATAACCCCACAGGAATCCCAT	240
sota.flu	CAGCCGTTCACCTGCTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
del.leu	TAGCCGTCATTTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
mono.mon	TGGCCGTCACCTTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
plat.gan	CAATTATCCACCTACTATTCTACACGAAACAGGCTCAAACAAACCCCACAGGAATCCCAT	240
plat.min	CAGTTATCCACCTRACTATTCTACACGAAACAGGCTCAAACAAACCCCACAGGAATCCCAT	240
kogi.bre	CAATGGTCCACCTCTTATTCTACACGAAACAGGATCCAACAACCCCCTAGGAATCTTT	240
kogi.sim	CAATAATCCACCTCTTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCCT	240
phys.cat	CAATAGTACATCTCTTATTCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCCT	240
lipo.vex	CAACCCTCCACCTACTATTCTCATGAAACAGGATCCAACAACCCCCTAGGAATCCCCT	240
phoc.sin	TAATCGTCATCTACTATTCTCCATGAAACAGGATCCAACAACCCCACAGGAATCCCCT	240
bera.bai	CAGCCGTCACCTACTATTCTCCACGAAACAGGATCCAACAACCCCACAGGAATCCCCT	240
ziph.car	CAGCCGTCACCTACTATTCTCCACGAAACAGGATCTAATAACCCCACAGGAATCCCCT	240
meso.eur	CAATCGTCACCTACTATTCTCCATGAAACAGGATCCAATAACCCCACAGGAATCCCCT	240
meso.bid	CAATCGTCACCTACTATTCTCCATGAAACAGGATCTAATAACCCCACAGGAATCCCCT	240
meso.den	CAATCGTCACCTACTATTCTCCATGAAACAGGATCTAATAACCCCACAGGAATCCCCT	240
hype.amp	CAATCGTCACCTACTATTCTCCATGAAACAGGATCTAATAACCCCCTAGGAATCTCTT	240
meso.ger	CAATTGTCATTTACTATTCTACACGAAACAGGATCTAACAACCCCCTAGGAATCTCAT	240
poat.bla	TTATAGTCACCTGCTATTCTACACGAAACTGGATCTAACAAACCCCACAGGAATCTCAT	240
hex.lib	CCGCCGTCACCTACTTTCTCCACGAAACAGGCTCAAACAAACCCCACAGGAATCTCAT	240
hipp.amp	CCATCGTCATCTACTATTCTCATGAAACAGGATCTAACACCCCCTAGGAATCTCAT	240
dic.sum	CAATTACCCACCTGCTATTCTACACGAAACAGGATCTAACACCCCCTAGGAATCTCAT	240
chin.sen	CGATCACCCACTTACTATTCTACACGAAACAGGATCTAACACCCCCTAGGAATCTCAT	240
cera	CAATCACCCACCTACTATTCTCATGAAACAGGATCTAACACCCCCTAGGAATCTCAT	240
equu	TAATCGTCATCTACTATTCTCATGAAACAGGATCTAACACCCCCTAGGAATCTCAT	240
baby.bab	CAACCGTACATCTATTCTCATGAAACAGGATCTAACACCCCCTAGGAATCTCAT	240
phac.aec	CAACCGTACATCTTCTCATGAAACAGGATCTAACACCCCCTAGGAATCTCAT	240
sus.bac	CAGCCSTACATCTCTTACGAAACAGGATCTAACACCCCCTAGGAATCTCAT	240
sus.scc.swb1	CAGCCSTACATCTCTTACGAAACAGGATCTAACACCCCCTAGGAATCTCAT	240

lama.gla	CAGGAGTACATCTACTATTTTACACGAAACAGGCTCCAACAATCCAACAGGAATTCTT	240
lama.gua	CAGGAGTCCATCTACTATTTTACACGAAACAGGCTCCAACAATCCAACAGGAATTCTT	240
vic.vic	CGGGAGTACATCTACTATTTTACACGAAACAGGCTCCAACAATCCAACAGGAATTCTT	240
cam.bac	TAGCCGTACACCTATTTCCTACACGAAACAGGCTCAATAACCCGACAGGAATCTCCT	240
arc.for	TAATAGTACATCTGCTATTCCCTACATGAAACAGGATCCAATAACCCATCAGGAGTCTCCT	240
arc.gaz	TAATAGTGCACCTACTATTCCCTACACGAAACAGGATCCAACAACCCATCAGGAGTCTCCT	240
eum.jub	TAATAGTACACCTATTTCCTACACGAAACTGGATCCAACAACCCATCAGGAATCTCCT	240
zal.cal	TAATAGTACACCTATTTCCTACACGAAACAGGATCTAACACACCCCTCGGGAAATCTCCT	240
odo.ros	CAGCAGTACACCTACTATTCCTACACGAAACAGGATCCAACAACCCCTCGGGAAATCTCCT	240
pho.fasciata	CGGCAGTTCACCTACTATTCCTACACGAAACAGGATCCAACAACCCCTCGGGAAATCTCCT	240
pho.gro	CGGCAGTTCATCTACTATTCCCTACACGAAACAGGATCCAACAACCCCTCGGGAAATCTCCT	240
pho.vit	CAGCAGTCCACCTACTATTCCTACACGAAACAGGATCCAACAACCCCTCGGGAAATCTCCT	240
cys.cri	CAACAGTCCACCTACTATTCCTACACGAAACAGGATCTAACACCCCTCGGGAAATCTCCT	240
hyd.lep	CAGCAGTACATCTACTATTCCTACACGAAACAGGATCCAACAACCCCTCGGGAAATCTCCT	240
lep.wed	CAGCAGTACATCTACTATTCCTACACGAAACAGGATCCAACAACCCCTCTGGAATCTCCT	240
mir.leo	CAGCAGTACATCTACTATTCCTACACGAAACAGGATCCAACAACCCCTCTGGAATCTCCT	240
eri.bar	CAGCAGTCCACCTATTTCCTACACGAAACAGGATCCAACAACCCCTCTGGAATCTCCT	240
mon.sch	CAGCAGTCCATTTATTTCCTACACGAAACAGGATCCAACAACCCCTCGGGAAATCTCCT	240
hela.mal	CAGCGGTCCACCTATTTCCTACACGAAACAGGATCCAACAACCCCTCTGGAATCTCCT	240
sel.thi	CAGCAGTTCATCTATTGTTCTACACGAAACAGGATCCAACAACCCCTCTGGAATCTCCT	240
ail.ful	CAACTATCCATCTCTATTCCCTACATGAAACAGGATCTAACACCCCTCAGGCAATCTCCT	240
fel.	CAGGAGTACACCTCTATTCCCTCATGAAACAGGATCTAACACCCCTCAGGAATTACAT	240
can	CAATAGTACACCTCTATTTCCTACACGAAACCGGATCCAACAACCCCTCAGGAATCTCCT	240
tal	CTGGAGTTCACCTGTTATTTCCTCACGAAACAGGATCCAACAACCCATCAGGACTCTCCT	240
gla.sab	CCATAATCCATCTACTCTTTCACACGAAACAGGATCCAATAACCCATCAGGACTAATCT	240
gla.vol	CCATAATCCATCTACTCTTTCACACGAAACAGGATCCAATAACCCATCAGGCCCTAATTCT	240
byl.pha	CTATAATCCACCTTCTCTTTCACACGAAACAGGATCCAATAACCCATCAGGCTCTAATTCT	240
pet.set	CTATAATCCACCTTCTCTTTCACACGAAACAGGATCCAATAACCCATCAGGCTCTAATTCT	240
bel.pea	CAATAGTCACCTTCTTTCCTCCACGAAATTGGGTCAAATAACCCCCCGGAAATTCTCCT	240
pte.mom	CAATAGTTCACCTACTTTTCCTCATGAAACAGGATCCAACAACCCATCTGGACTTACCT	240
gala.demi	TCATAATCCACCTCTTTCCTCACGAAACAGGATCAAACAACCCATCAGGACTCTCCT	240
pero.poc	CCACAACTCACCTCTTTCCTCACGAAACAGGATCAAATAACCCATCAGGAGAATTCTCCT	240
gala.mat	CCATAATTCCACCTTCTTTCCTACATGAAACAGGATCAAACAACCCCTCAGGAATCTCCT	240
gala.moh	CCATAATTCCACCTTCTTTCCTACATGAAACAGGATCAAACAACCCATCTGGGAATCTCCT	240
oto.gar	TCATAATCCACCTTCTTTCCTCACGAAATCAGGATCAAATAACCCATCAGGCTCTAATTCT	240
lor.tat	CTGCAATTTCACCTACTTTTCCTACACGAAATCAGGATCAAATAACCCATCAGGGAATTCTCCT	240
nyc.cou	TTGTGATTTCACCTCATCTTTCCTACATGAAACAGGATCAAATAACCCATCAGGAAATTCTCCT	240
mus	CAATCGTTCACCTCTTTCCTCACGAAACAGGATCAAACAACCCATCTGGCATCTCCT	240
gorr	CAACCCCTCCATCTCTTTCCTACACGAAACAGGATCAAACAACCCCTCTAGGCATCTCCT	240
homo	CAACACTCCACCTCTTTCCTACATGAAACAGGATCAAACAACCCCTCTAGGAATCTCCT	240
dug.dug	TAATAGTCACCTACTATTCCTCACGAAACAGGCTCAAACACCCACTGGGACTCTCCT	240
ele.max	CAGGAGTGCACCTAACCTTCTCACGAAACAGGCTCAAACACCCACTAGGTCTCCT	240
afr.con	CAATTATCCACCTCACATTCTCATGAAATCAGGCTCAAACACCCACTGGGACTCTCCT	240
pavo.mut	CAATTATCCACCTCACATTCTCATGAAATCAGGCTCAAATAACCCACTAGGCATCTCCT	240
tra.bily	CCATCATGCACCTCATCTTCTACATGAAATCAGGCTCAAACACCCACTGGGACTCTCCT	240
tra.sae	CTATCATACACCTCATCTTCTACATGAAATCAGGCTCTAACACACCCCTGGGACTCTCCT	240
tra.cob	CCATCATCCACCTCATCTTCTACATGAAATCAGGCTCAAACACCCACTGGGACTCTCCT	240
tra.tem	CCATCATCCACCTCATCTTCTACATGAAATCAGGCTCAAACACCCACTGGGACTCTCCT	240
arg.arg	CCATCATCCACCTCACATTCTACACGAAATCAGGCTCAAACACCCACTGGGACTCTCCT	240
cat.wal	CCATCACCCCATCTCATATTCTACATGAAATCAGGCTCAAACACCCACTGGGACTCTCCT	240
cro.cro	CTGTCAACCCACCTCATATTCTACACGAAATCAGGCTCAAACACCCACTAGGCATCTCCT	240
sym.zee	CCATCACACATCTTACACGAAATCAGGCTCAAACACCCACTAGGCATCTCCT	240
bam.tho	CCATTATCCACCTCACATTCTACACGAAATCAGGCTCAAACACCCACTGGGACTCTCCT	240
sea.fra	CTATCATCCACCTCACATTCTGACGAAATCAGGCTCAAACACCCACTGGGACTCTCCT	240
ith.cri	CTGTCAACCCACCTCATATTCTACACGAAATCAGGCTCAAACACCCACTAGGCATCTCCT	240
int.pac	CCCTAATCCACCTCACCTTACACGAAATCAGGCTCAAACACCCACTGGGACTCTCCT	240
int.vic	CCCTAATCCACCTCACCTTACACGAAATCAGGCTCAAACACCCACTGGGACTCTCCT	240
scut.anc	CCCTAATCCACCTCACCTTACACGAAATCAGGCTCAAACACCCACTGGGACTCTCCT	240

gru.ant.gil	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT	240
gru.ant.sha	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT	240
gru.leu	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT	240
gru.can.pra	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT	240
gru.can.row	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAATCCCCTAGGCATTGTAT	240
gru.can.tab	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCTAGGCATTGTAT	240
gru.can.can	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCTAGGCATTGTAT	240
gru.ame	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT	240
gru.gru	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT	240
gru.mon	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT	240
gru.nig	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT	240
gru.jap	CCCTAATCCACCTCACCTTCTTACGAGTCGGCTCAAACAACCCCCTAGGCATCATCT	240
cic.boy	CCTTATCCACCTCACCTTCTTACGAAACCGGGTCAAACAAACCCCCTAGGAATCGTAT	240
rhe.ame	TCTTAATTCACTGGCATTCCTCACGAATCAGGCTCAAACAACCCACTAGGCATCACAT	240
ant.alb	CCTTAATTCACTTCACCTTCTTACATGAATCAGGTTCAAACAAACCCCCTAGGAATCACAT	240
fal.fam	CCTTAATTCACTTCACCTTCTTACCGAATCAGGTTCAAACAAACCCCCTAGGAATCACAT	240
fal.ver	CCTTAATTCACTTCACCTTCTTACATGAATCAGGCTCAAATAAACCCCCTAGGAATCACAT	240
fal.per	CCTTAATTCACTTCACCTTCTTACATGAATCAGGTTCAAACAAACCCCCTAGGAATCACAT	240
fal.spa	CCCTAGTCCACCTAACCTTCTGACGAGTCAGGCTCAAACAAACCCCCTAGGCATTGTAT	240
ayt.ame	CACTCATCCATCTCACCTTCTCATGAAACAGGTTCAAACAAACCTCTAGGTATCTCAT	240
smi.sha	CTCTAGTCCACCTCACATTCTCACGAAACAGGATCAAACATCCATAGGAATTCCAT	240
vid.cha	CAATAGTACACCTACTTTCTACATGAAACTGGATCAAACAAACCCACAGGATTAAACT	240
chry.pic	CAATAGTACACCTACTCTTCTCACGAAACCGGATCAAACATCCACAGGATTAAACT	240
emy.orb.kur	CAGCACTACATCTATTATTCTGACGAAACAGGATCAAACAAACCCACAGGACTAAATT	240
che.mud	CAATAATTCACTACTATTCTCACGAAACAGGATCAAATAACCCACCGGACTAAATT	240
eum.egr	*****	*

aep.mel	CAGATTCAAGATAAAATTCCATTCCACCCCTACTATACTATTRAAGAGACATCCTAGGAATCC	300
ore.ore	CAGACACAGACAAAATTCCATTTCATCCTTATTACACAAATCAGAGATATCCTAGGCGCCC	300
add.nas	CAGACACAGACAAAATTCCATTCCACCCCTACTATACTACATTAAAGACATCTTAGGCGCCC	300
ory.dam	CAGACACAGACAAAATTCCGTTCCACCCCTATTATACCATTAAGAGATATCTTAGGCGCCC	300
hip.equ	CAGACTCCGATAAAACCCATTCCACCCCTACTACACCATTAAAGACATCTTAGGCGCCC	300
alc.bus	CRAGCCGAGATAAAATTCCATTCCACCCCTACTATACTACATCAGGACATTCTAGGCGCCC	300
sig.lic	CAGACGGAGATAAAATTCCATTCCACCCCTACTATACTACAGGACATTCTAGGCGCCC	300
bea.hun	CAGATGCAGATAAAATTCCATTCCACCCCTACTACACCATTCAAAGACATCCTAGGCGCCC	300
dam.lun	CAGATGCCGACAAAATTCCGTTCCACCCCTACTACACTATCAAAGACGCCCCCTAGGGGCC	300
con.cau	CCGACACCGATAAAATTCCATTCCCCCTATTACACCATCAAAGACATCCTAGGCGCTC	300
amm.ler	CAGACGGAGACAAAATTCCATTCCACCCCTACTACACCATCAAAGAGATATTCTAGGCGCCA	300
pse.nay	CAGACACAGACAAAATTCCATTCCACCCCTACTACACCATCAAAGAGATATTCTAGGCGCTG	300
cap.ibe	CAGACACAGACAAAATTCCATTCCACCCCTACTACACCATCAAAGAGATATTCTAGGCGCCA	300
hem.jem	CAGATACAGACAAAATTCCATTCCACCCCTACTACACCATCAAAGAGATATTCTAGGCGCCA	300
cap.fal	CAGACACAGACAAAATTCCATTCCACCCCTACTACACCATCAAAGAGATATTCTAGGCGCCA	300
rup.pyr	CAGATGCCGATRAAAATTCCATTCCACCCCTACTATACTACATTAAAGAGATATTCTGGGGGCC	300
rup.rup	CAGATGCCGACAAAATTCCATTCCACCCCTATTATACCATCAAAGAGATATTCTAGGCGCTA	300
nem.cau	CAGACATAGACAAAATTCCATTCCACCCCTATTATACCATCAAAGAGATATTCTAGGAGCTA	300
bud.tax.tax	CAGATGCCAGATAAAATTCCATTCCACCCCTATTACACCATCAAAGAGATATTCTAGGCGCTA	300
pan.hod	CAGATCCAGACAAAATTCCATTCCACCCCTACTATACTACACCATCAAAGAGATCTTAGGCGCTA	300
ovi.amm	CGGACACAGATAAAATTCCCTTCCACCCCTACTACACCATCAAAGAGATCTTAGGCGCTA	300
ovi.vig	CGGACACAGACAAAATTCCCTTCCACCCCTACTACACCATCAAAGAGATCTTAGGCGCTA	300
cap.cri	CAGACACAGACAAAATTCCATTCCACCCCTACTACACCATCAAAGAGATCTTAGGCGCTA	300
ovi.mos	CAGACACAGACAAAATTCCATTCCACCCCTACTACACCATCAAAGAGATCTTAGGCGCTA	300
ore.ame	CAGACCGAGACAAAATTCCATTCCACCCCTACTACACCATCAAAGAGATCTTAGGCGCTA	300
cep.dor	CGGACCGAGACAAAATTCCATTCCACCCCTACTACACCATCAAAGAGACATCCTAGGCGCC	300
cep.max	CAGACCGAGACAAAATTCCATTCCACCCCTACTACACCATCAAAGAGACATCCTAGGAGCT	300
bis.bon	CAGACCGAGACAAAATTCCATTCCACCCCTACTACACCATCAAAGAGACATCCTAGGAGCT	300
bos.gru	CAGACCGAGACAAAATTCCATTCCACCCCTACTACACCATCAAAGAGACATCTAGGAGCT	300
bon.bra	CAGACCGAGACAAAATTCCATTCCACCCCTACTACACCATCAAAGAGACATCTAGGAGCT	300

bub.min	CACACACAGACAAAATCCCATTCCACCCCTACTACACCATAAGACATTCTAGGGCCCC	300
buba.bub	CAGACACAGACAAAATCCCATTCCACCCCTATTACACCATAAGACATTCTAGGGCCCC	300
tra.ang	CAGACATAGACAAAATCCCATTCCACCCCTATTACACTATAAGGACATTCTAGGGCCCC	300
tra.eur	CRAACATAGACAAAATCCCATTCCACCCCTACTACACTATAAGGACATTCTAGGTGGCC	300
kob.ell	CAGACATAGACAAAATCCCATTCCACCCCTACTACACCATAAGACATTCTAGGGCCCC	300
kob.meg	CAGACACAGACAAAATCCCATTCCACCCATATTACCATATAAGGACATTCTAGGGCCCC	300
zed.aru	CAGATGTAGACAAAATCCCATTCCATCCATACTATACTATAAGGACGTCTAGGGCCCC	300
zed.ful	CAGAYATGGACAAAATCCCATTCCACCCNTACTACACCATAAGGACATTCTAGGTGGCC	300
neo.mos	CAGACCGAGACAAAATCCCATTCCACCCCTACTACACCATAAGACATTCTAGGGCCCC	300
pel.cap	CCGACATAGACAAAATCCCATTCCACCCATACTACACCATAAGGATATTCTAGGGCCCC	300
gaz.dam	CAGATGCAGACAAAATCCCCTTCCACCCCTACTACACCATAAGGACATTCTAGGAGCAC	300
our.our	CAGATGCAGACAGGTCCCCATTCCACCCCTACTACACCATAAGACATTCTAGGGCCCC	300
ant.cer	CAGACCGAGACAAAATCCCATTCCACCCCTACTACACTATAAGGATATTCTAGGGCCCC	300
sai.tat	CAGATTCAAGACAAAATCCCATTCCACCCCTACTACACCATAAGGACATTCTAGGGCCCC	300
mad.kir	CAGACCGAGACGGAAATCCCATTCCGGCCCCCTACTACACTATAAGGACATTCTAGGGCCCC	300
rap.mel	CAGATATAGACAAAATCCCATTTCACCCCTACTACACCATAAGGACATTCTAGGAGGCC	300
gaz.gaz	CAGACCGAGACAAAATCCCATTTCACCCCTACTACACCATAAGGACATTCTAGGAGCAC	300
ant.ame	CAGACCGAGACAAAATCCCATTTCACCCCTACTACACCATAAGGACATTCTAGGAGCAC	300
hyd.ine	CAGATGCAGATAAATTCCCATTTCATCCCTACTACACCATAAGGATATTCTAGGTGTAC	300
mun.mun	CAGATGTAGACAAAATTCCCTTCCACCCCTACTACACCATAAGGATATTCTAGGTGGCC	300
alc.alc	CAGACGGAGACAAAATCCCATTTCACCCCTACTACACCATAAGGATATTCTTAGGCATCT	300
cer.el.a.kan	CAGACGGAGACAAAATCCCCTTCCATCCCTACTACACCATAAGGATATTCTTAGGCATCT	300
cer.el.a.xan	CAGACGGAGACAAAATCCCCTTCCACCCCTACTACACCATAAGGATATTCTTAGGCATCT	300
cer.el.a.can	CAGACGGAGACAAAATCCCCTTCCATCCCTACTACACCATAAGGATATTCTTAGGCATCT	300
cer.nip.cent	CAGACGGAGACAAAATCCCCTTCCATCCCTACTACACCATAAGGATATTCTTAGGCATCT	300
cer.nip.yes	CAGACGGAGACAAAATCCCCTTCCATCCCTACTACACCATAAGGATATTCTTAGGCATCT	300
cer.nip.ker	CAGACGGAGACAAAATCCCCTTCCATCCCTACTACACCATAAGGATATTCTTAGGCATCT	300
cer.nip.pul	CAGACGGAGACAAAATCCCCTTCCATCCCTACTACACCATAAGGATATTCTTAGGCATCT	300
cer.nip.nip	CAGACGGAGACAAAATCCCCTTCCATCCCTACTACACCATAAGGATATTCTTAGGCATCT	300
cer.el.a.sco	CAGATGTAGATAAATTCCCCTTCCATCCCTACTACACCATAAGGATATTCTAGGTGTCC	300
cer.dam	CAGACTCAGATAAATTCCCATTCCATCCCTATTACACTATAAGGACATTCTAGGCATCC	300
tan.car	CAGATATAGACAAAATCCCATTCCACCCCTACTACACCATAAGGACATTCTAGGTGTCC	300
mos.fus	CAGATATAGACAAAATCCCATTCCACCCCTACTACACCATAAGGACATTCTAGGTGTCC	300
mos.leu	CAGATATAGACAAAATCCCATTCCACCCCTACTACACCATAAGGACATTCTAGGTGTCC	300
mos.chr	CAGACATAGACAAAATCCCATTCCACCCCTACTACACTATAAGGACATTCTAGGTGTCC	300
mos.bez	CAGACATAGACAAAATCCCATTCCACCCCTACTACACCATAAGGATATTCTAGGTGTCC	300
mos.mos	CAGACATAGACAAAATCCCCTTCCACCCCTACTACACCATAAGGACATTCTAGGGGTTC	300
tra.jav	CAGACCGAGACAAAATCCCCTTCCACCCCTACTACACCATAAGGATATTCTAGGGGTTC	300
trag.nap	CAGACCGAGACAAGATCCCCTTCCACCCCTACTACACCATAAGGACATTCTAGGGCCCC	300
bala.acu	CTGACATAGACAAAATCCCATTCCACCCCTATTACACATAAGGACATTCTAGGGCCCC	300
bala.bon	CTGATATAGACAAAATCCCATTCCACCCCTATTACACATAAGGACATTCTAGGGCCCC	300
bala.bor	CCGACATAGACAAAATCCCATTCCACCCCTATTACACAGTTAAAGGACATTCTAGGGCCCC	300
bala.edi	CCAACATAGACAAAATCCCATTCCACCCCTATTACACACTAAAGGACATTCTAGGGCCCC	300
esch.rob	CCAACATAGACAAAATCCCATTCCACCCCTATTACACACTAAAGGACATTCTAGGGCCCC	300
bala.mus	CTGACATAGATAAAATCCCATTCCACCCCTATTACACACTAAAGGACATTCTAGGGCCCC	300
mega.nov	CCAACATAGACAAAATCCCATTCCACCCCTATTACACACTAAAGGACATTCTAGGGCCCC	300
bala.phy	CCGACATAGACAAAATCCCATTCCACCCCTATTACACACAAATTAAAGGACATTCTAGGGCCCC	300
cap.mar	CCAACATAGACAAAATCCCATTCCACCCCTATTACACACAAATTAAAGGACATTCTAGGGCCCC	300
ceph.com	CCAACATAGACATAATCCCATTCCACCCCTATTACACACAAATTAAAGGACATTCTAGGGCCCC	300
ceph.eut	CCAACATAGACATAATCCCATTCCACCCCTATTACACACAAATTAAAGGACATTCTAGGGCCCC	300
lage.col	CCAACATAGACATAATCCCATTCCACCCCTATTACACACAAATTAAAGGACATTCTAGGGCCCC	300
ceph.hea	CCAACATAGACATAATCCCATTCCACCCCTATTACACACAAATTAAAGGACATTCTAGGGCCCC	300
ceph.hed	CCAACATAGACATAATCCCATTCCACCCCTATTACACACAAATTAAAGGACATTCTAGGGCCCC	300
lage.ais	CCAACATAGACATAATCCCATTCCACCCCTATTACACACAAATTAAAGGACATTCTAGGGCCCC	300
lage.zru	CCAACATAGACATAATCCCATTCCACCCCTATTACACACAAATTAAAGGACATTCTAGGGCCCC	300
lage.zbs	CCAACATAGACATAATCCCATTCCACCCCTATTACACACAAATTAAAGGACATTCTAGGGCCCC	300
lisse.boc	CCAACATAGACATAATCCCATTCCACCCCTATTACACACAAATTAAAGGACATTCTAGGGCCCC	300
lisse.pac	CCAACATAGACATAATCCCATTCCACCCCTATTACACACAAATTAAAGGACATTCTAGGGCCCC	300

glo.mac	CCAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGACATCCTAGGGGCC 300
glo.mel	CCAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGACATCCTAGGGGCC 300
fere.att	CCAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGACATCCTAGGTGCC 300
pepo.ele	CCAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGACATCCTAGGGGCC 300
gram.gri	CCAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGACATCCTAGGGGCC 300
pse.cra	CCAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGACATCCTAGGGGCC 300
lage.acu	CTAACATAGATATAATCCGTTCCACCCCTATTATAACAATTAAAGACATCCTAGGGGCC 300
orci.bre	CCAACATAGATATAATCCATTCCACCCCTATTACACATTAAAGACATCCTAGGGGCC 300
orca.bre	CCAACATAGACATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGGGCC 300
del.cap	CCAATATAGACATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTGCC 300
del.tro	CCAATATAGACATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTGCC 300
del.del	CCAATATAGACATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTGCC 300
sten.cly	CCAATATAGACATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTGCC 300
sten.coe	CCAATATAGACATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTGCC 300
tur.adu	CCAATATAGACATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTGCC 300
sten.fro	CCAATATAGACATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTGCC 300
saus.chi	CCAACATAGACATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTGGCT 300
sten.lon	CCAACATAGACATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTGCC 300
turs.tru	CCAACATAGATATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTGCC 300
lage.alb	CCAACATAGATATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTGCC 300
sten.bre	CCAACATAGATATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTGCC 300
sota.flu	CCAACATAGATATAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTGCC 300
del.leu	CCAACATGGATACAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
mono.mon	CCAACATAGACATAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
plat.gan	CCGACACTGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACACCCCTAGGGGCC 300
plat.min	CCAACACTGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
kogi.bre	CCGACATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
kogi.sim	CTGATATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGTGCC 300
phys.cat	CCAACATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACACCCATAGGTGCC 300
lipo.vex	CTAACATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
phoc.sin	CTAACATAGACATAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
bera.bai	CCAATATAGATAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
ziph.cat	CCGATATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACACCTTAGGGGCC 300
meso.eur	CTGATATAGACAAAAATTCCATTCCCATCTTACTACACATTAAAGACATCCTAGGGGCC 300
meso.bid	CCGACATAGATAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
meso.den	CTGACATAGATAAAAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGGGCC 300
hype.amp	CTGACATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
meso.per	CTGACATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
ponc.bla	CTAACATAGATGCCATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
hex.lib	CAAACGGCAGACAAAAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTAC 300
hipp.amp	CAAACGGCAGACAAAAATTCCATTCCACCCCTATTACACATTAAAGACATCCTAGGTAC 300
dic.sum	CTAACATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
shin.son	CTAACACAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
cera	CCAACATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
equu	CTGACATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
baby.bab	CACATATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
phac.aff	CACACATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
sus.bat	CACACATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
sus.sct.ewb3	CACACATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
lama.gla	CGGATATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
lama.gua	CGGATATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
vic.vic	CACATATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
cim.bat	CACACATAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
acc.fec	CTGACTGAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
acc.gaz	CTGACTGAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
eum.jub	CCAACTGAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
sal.cal	CTGACTGAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300
edi.coo	CTGACTGAGACAAAAATTCCATTCCACCCCTACTACACATTAAAGACATCCTAGGGGCC 300

pho.fasciata	CCGACTCAGACAAAATCCCATTCCACCCATACTATAACAATTAAAGATATCTAGGAGCCC	300
pho.gro	CCGACTCAGACAAAATCCCGCTCCACCCATACTATAACAATTAAAGATATCTAGGAGCCC	300
pho.vic	CCAACTCAGACAAAATCCCATTCCACCCATACTATAACAATTAAAGATATCTAGGGGCC	300
cys.cri	CCGACTCAGACAAAATCCCATTCCACCCATACTATAACAATTAAAGACATCTAGGAGCCC	300
hyd.lep	CCAACTCAGACAAAATCCCATTCCACCCATACTACACAATCAAAGACATCTAGGAGCCC	300
lep.wed	CTGACTCAGACAAAATCCCATTCCACCCATACTACACAATCAAAGACATCTAGGAGCCC	300
mir.leo	CCGACTCAGACAAAATCCCATTCCACCCATACTACACAATCAAAGACATCTAGGAGCCC	300
eri.bar	CCGACTCAGATAAAAATCCCATTCCACCCATACTATAACAATTAAAGACATCTAGGAGCTT	300
mon.sch	CCAACTCAGACAAAATCCCATTCCACCCATACTATAACAATTAAAGACATCTAGGCGCC	300
hela.mal	CTGACTCAGACAAAATCCCATTCCACCCATACTACACAATCAAAGATATCTTAGGAGCCC	300
sel.thi	CCAACTCGGACAAAATCCCATTCCACCCATACTATAACAATTAAAGACGCCCTAGGCGCC	300
ail.ful	CCAACTCAGACAAAATCCCATTCCACCCATACTATAACAATTAAAGACATCTAGGTCTTC	300
fel	CCGATTCAAGACAAAATCCCATTCCACCCATACTATAACAATTAAAGACATCTAGGAGCT	300
can	CAGACTCAGACAAAATCCCATTCCACCCATACTACACAATCAAAGGATATCTAGGAGCAC	300
tal	CAGATACTGGATAAAAATCCCATTCCACCCATACTACACAATTAAAGACATCTAGGAGCAC	300
gla.sab	CTGACTCAGATAAAAATCCCATTCCACCCATACTATAACAATTAAAGACACCCTAGGATTCT	300
gla.vol	CTGACTCAGACAAAATCCCATTCCACCCATACTATAACAATTAAAGATATCTGGCGCTC	300
hyl.pha	CCGATTCAAGACAAAATCCCATTCCACCCATACTATTCAATTAAAGATCTCTAGGAGCCC	300
pet.set	CCGATTCAAGACAAAATCCCATTCCACCCATACTATTCAATTAAAGATCTCTAGGGGCC	300
bel.pea	CTGAATCTGATAAAAGTACCATCCACCCATACTTCACAAATCAAAGATATTCTGGCGCC	300
pse.mom	CCGAATCCGACAAAATCCCATTCCACCCATACTTCACAAATTAAAGACATTITAGGAGCAC	300
gala.demi	CAGACTCAGACAAAATCCCCTTCAACCCATACTACACAATCAAAGGATCTCTAGGACTGA	300
pero.pot	CAGAATCAGACAAAATCCCCTTCAACCCATACTACACCAAAAGACTTACTAGGAGCA	300
gala.mat	CAGACTCCGACAAAATCCCATTCCACCCATACTACACAATTAAAGACCTACTAGGAGTA	300
gala.moh	CAGACTCCGACAAAATCCCCTTCAACCCATACTACACAATTAAAGACCTACTAGGAGCA	300
oco.gar	CAGACTCTGACAAAATCCCCTTCAACCCATACTACACAATTAAAGACCTTCTAGGGCTA	300
lor.tar	CAGACTCTGACAAAATCCCATTCCACCCATACTACACAATTAAAGATATTCTAGGAGTA	300
nyc.cou	CAGACTCAGATAAGATTCCATTCCACCCATACTACTCACTTAAGACCTCTAGGAGTGG	300
mus	CAGATGAGATAAAAATCCCATTCCACCCATACTATAACAATTAAAGATATCTAGGTATCC	300
gorr	CCCACTCTGACAAAATCCCCTTCAACCCATACTACACAATTAAAGACATCTAGGCTTAT	300
homo	CCCAATTCCGATAAAAATCCCCTTCAACCCATACTACACAATTAAAGACGCCCTGGCTTAC	300
dug.dug	CCGACTCAGACAAAATCCCATTCCACCCATAATTATTCACTGAAAGACCTCTAGGCTTAT	300
ele.max	CAGACTCAGACAAAATCCCCTTCAACCCATACTACACAATTAAAGACTTACTAGGCTAC	300
afr.con	CCAATTCAAGATAAAAATCCCATTCCACCCGTACTACTCCCTCAAAGATATCTAGGCTTA	300
pavo.mut	CCAACTCAGACAAAATCCCATTCCACCCATACTACTCCCTCAAAGATATCTGGGTCTAA	300
tra.bly	CTAACTCTGACAAAATCCCATTCCACCCATACTACTCCCTCAAAGATATCTGGGTCTAA	300
tra.sat	CCAACTCTGACAAAATCCCATTCCACCCATACTACTCCCTCAAAGATATCTAGGCTTAA	300
tra.cob	CTGACTCTGACAAAATCCCATTCCACCCGTACTACTCCCTCAAAGATATCTGGGTCTAA	300
tra.tem	CTAACTCTGACAAAATCCCATTCCACCCATACTACTCCCTCAAAGATATCTAGGCTTAA	300
arg.arg	CTAACTCTGACAAAATCCCATTCCACCCATACTACTCCCTCAAAGATATCTAGGCTTAA	300
cat.wal	CTAAATTCCGACAAAATCCCATTCCACCCATACTACTCCCTCAAAGACATCTAGGCTTAG	300
cro.cro	CTAAACTCTGACAAAATCCCATTCCACCCATACTACTCTCTCAAAGATATCTAGGCTTAG	300
sym.ree	CTAAACTCTGACAAAATCCCATTCCACCCATACTACTCTCTCAAAGATATCTAGGCTTAG	300
bam.tho	CTGACTCTGACAAAATCCCATTCCACCCATACTACACCCCTCAAAGACATCTAGGCTTAA	300
fra.fra	CTAACTCTGACAAAATCCCATTCCACCCATACTACTCCCTCAAAGACATCTAGGCTTAG	300
ith.cru	CAAACCTGGGATAAAAATCCCATTCCACCCATACTACTCTCTCAAAGATATCTAGGATTCA	300
ant.par	CAAACCTGGGATAAAAATCCCATTCCACCCATACTACTCTCTCAAAGATATCTAGGATTCA	300
ant.vir	CAAACCTGGGATAAAAATCCCATTCCACCCATACTCTTTCTCAAAGATATCTAGGATTCA	300
gru.ant.ant	CAAACCTGGGATAAAAATCCCATTCCACCCATACTCTTTCTCAAAGATATCTAGGATTCA	300
gru.ant.gil	CAAACCTGGGATAAAAATCCCATTCCACCCATACTCTTTCTCAAAGATATCTAGGATTCA	300
gru.ant.sha	CAAACCTGGGATAAAAATCCCATTCCACCCATACTCTTTCTCAAAGATATCTAGGATTCA	300
gru.leu	CAAACCTGGGATAAAAATCCCATTCCACCCATACTCTTTCTCAAAGATATCTAGGATTCA	300
gru.can.pra	CAAACCTGGGATAAAAATCCCATTCCACCCATACTCTTTCTCAAAGATATCTAGGATTCA	300
gru.can.cow	CAAACCTGGGATAAAAATCCCATTCCACCCATACTCTTTCTCAAAGATATCTAGGATTCA	300
gru.can.tab	CAAACCTGGGATAAAAATCCCATTCCACCCATACTCTTTCTCAAAGATATCTAGGATTCA	300
gru.can.san	CAAACCTGGGATAAAAATCCCATTCCACCCATACTCTTTCTCAAAGATATCTAGGATTCA	300
gru.jame	CAAACCTGGGATAAAAATCCCATTCCACCCATACTCTTTCTCAAAGACATCTAGGATTCA	300
gru.jen	CAAACCTGGGATAAAAATCCCATTCCACCCATACTCTTTCTCAAAGATATCTAGGATTCA	300

gru.mon	CAAACTGGGATAAAAATCCATTCCACCCCTATTTTCTTAAAGATATCCTAGGATTCA	300
gru.nig	CAAACTGGGATAAAAATCCATTCCACCCCTATTTTCTTAAAGATATCCTAGGATTCA	300
gru.jap	CAAACTGTGATAAAAATCCCATTCCACCCCTATTTTCTTAAAGATATCCTAGGATTCA	300
cic.boy	CAAACTGGCACA AAAATCCATTCCACCCCTACTTCTCCCTCAAAGATATCCTAGGATTCA	300
rhe.ame	CTCACTCTGACAAAATCCCATTCCACCCCTACTTCTCCCTAAAGATGCCTAGGACTAG	300
ant.alb	CCAACCTGGCACA AAAATCCCATTCCACCCCTACTTGCCTAAAGACATCCTAGGATTCA	300
fal.fam	CAAACTGGGATAAAAATCCCATTCCACCCCTACTTCTCCCTAAAGACATCCTAGGATTCA	300
fal.ver	CAAACTGGGACA AAAATCCCATTCCACCCCTACTTCTCCCTAAAGATATCCTAGGATTCA	300
fal.per	CAAACTGGGACA AAAATCCCATTCCACCCCTACTTCTCCCTAAAGACATCCTAGGATTCA	300
fal.spa	CAAACTGTGACAAAATCCCATTCCACCCCTACTTCTCCCTAAAGACCTCTAGGTTTA	300
ayt.ame	CAGACTGGCACA AAAATCCCATTCCACCCCTACTTCTCCCTAAAGACATCCTAGGATTCA	300
smi.sha	CTAACTCCGATAAAAATCCCATTCCACCCCTACTTCTCCATAAAAGACATTCTAGGTTTG	300
vid.cha	CAGACTGTGACAAAATCCCATTCCACCCCTACTACACCACAAAGGACATCCTAGGTTCG	300
chry.pic	CAAACACTGACAAAATCCCATTCCACCCCTATTCTCTATRAAGACCTTTAGGGCTCA	300
emy.orb.kur	CAAACACCGATAAAAATCCCATTCCACCCCTACTTCTCTATRAAGACCTATTAGGACTCA	300
che.mud	CAAATACCGACAAAATCCCATTCCACCCCTACTTCTCTATRAAGACTTACTAGGACTCA	300
eum.egr	CTAGCACAGATAAGGTGCCATTCCACCCCTATTACACATACAGACCTCTGGTTCA	300
	* * *	
aep.mel	TATTAATAATTCTAGTCCTAATACTCCTAGTACTATTCAACCCGACCTACTAGGAGACC	360
ore.ore	TATTACTAATTCTAGCTTATTACTCTTAGTATTATTCAACACCTGACCTACTTGGAGACC	360
add.nas	TACTACTAATTCTAGTCCTCATACTACTAGTACTATTCAACACCCGACCTACTTGGAGACC	360
ory.dam	TACTACTAATTCTAGCCCTTATGTTGCTAGTATTATCGCACCCGACCTACTTGGAGACC	360
hip.equ	TACTACTAATTCTAGCCCTCATACTACTAGTACTATTTCGCACCCGACCTACTTGGAGACC	360
alc.bus	TATTACTAATTCTAGCCCTCATACTACTAGTACTATTTCGCACCCGACCTGCTCGGAGACC	360
sig.lic	TATTACTAATTCTAGCCCTCATACTACTAGTACTATTTCGCACCCGACCTGCTCGGAGACC	360
bea.bun	TACTACTAATTCTAGCCCTCATATTACTAGTACTATTTCGCCCCGACCTGCTCGGAGACC	360
dam.lun	TACTACTAATTCTAGCCCTCATATTACTAGTACTATTTCGCCCCGATTTACTTGGAGACC	360
con.tau	TATTACTAATTCTAGCCCTCATATTACTAGTACTATTTCGCCCCGATTTACTCGGGGACC	360
amm.ler	TGCTACTAATTCTCACCCTCATACTACTAGTACTATTTCACCCGACCTACTCGGGAGACC	360
pse.nay	CACTGCTAATTCTCGCCCTGATATTACTAGTATTTCACCCGACCTACTCGGGAGACC	360
cap.ibi	TGCTACTAATTCTGTCTTAATTACTAGTACTATTTCACCCGACCTACTCGGGAGACC	360
hem.jem	TACTACTAATTCTGTCTTAATTACTAGTACTATTTCACCCGACCTACTTGGAGACC	360
cap.fal	TACTACTAATTCTCGCCCTGATGCTACTAGTACTATTTCACCCGACCTACTCGGGAGACC	360
rup.pyr	TACTACTAATTCTCACCCTTATTAATTACTAGTACTATTTCACCCGACCTACTCGGGAGACC	360
rup.rup	TACTACTAATTCTCACCCTTATTAATTACTAGTACTATTTCACCCGACTTACTTGGAGATC	360
nem.cau	TACTACTAATTCTCGTCTCATGTTGCTAGTACTATTTCACCCGACTTACTTGGAGACC	360
bud.tax.tax	TACTACTAATTCTCTTAATTACTAGTACTATTTCACCCGACCTACTCGGGAGACC	360
pan.hod	TCCTACTAATTCTCACCCTCATACTACTAGTACTATTTCACCCGACCTACTCGGGAGACC	360
ovi.amm	TCCTACTAATTCTCACCCTCATGCTGCTAGTACTATTTCACCCGACCTACTTGGAGACC	360
ovi.vig	TCCTACTAATTCTCACCCTCATGCTGCTAGTACTATTTCACCCGACCTACTTGGAGACC	360
cap.cri	TCCTACTAATTCTCACCCTCATACTACTAGTACTATTTCACCCGACCTACTCGGGAGACC	360
ovi.mos	TACTACTAATTCTTACCCCTTATTAATTACTAGTACTATTTCACCCGACCTACTTGGAGACC	360
ore.ame	TACTACTCATCCTCACCCTTATTAATTACTAGTACTATTTCACCCGACCTACTCGGGAGACC	360
cep.dor	TACTACTCATTCAGCCCTTAATTACTAGTACTATTTCACCCGACCTACTTGGAGACC	360
cep.max	TATTAATTATTCTAGCCCTTAATTACTAGTACTATTTCACCCGACCTACTCGGGAGATC	360
bis.bon	TATTAATTATTCTAATTCTAATTACTAGTACTATTTCACCCGACCTACTCGGGAGACC	360
bos.gru	TATTAATTATTCTAGCCCTTAATTACTAGTACTATTTCACCCGACCTACTCGGGAGACC	360
bos.tra	TACTACTTATTCTAGCCCTTAATTACTAGTACTATTTCACCCGACCTACTCGGGAGACC	360
bub.min	TGCTATTAAATTCTAGCCCTTAATTACTAGTACTATTTCACCCGACCTACTCGGGGACC	360
buba.bub	TACTATTAAATTCTAGCCCTTAATTACTAGTACTATTTCACCCGACCTACTCGGGAGACC	360
tra.ang	TACTATTAAATTCTAGCCCTTAATTACTAGTACTATTTCACCCGACCTACTCGGGAGACC	360
tra.eur	TACTGCTAATTCTCTAAACTCTAAACTCTGCTACTATTTCACCCGACCTACTCGGGAGACC	360
kob.ell	TACTACTAATTCTCTAAACTCTAAACTCTGCTACTATTTCACCCGACCTACTTGGAGATC	360
kob.meg	TCTTATTAAATTCTCTAAACTCTAAACTCTGCTACTATTTCACCCGACCTACTTGGAGACC	360
ced.aru	TACTGCTAATTCTCTAAACTCTAAACTCTGCTACTATTTCACCCGACCTACTCGGGAGATC	360
ced.ful	TACTACTAATTCTCTGGCCCTAACACTATTACTGCTACTATTTCACCCGACCTACTCGGGAGACC	360
nco.moc	TCCTACTAATTCTCTAAACTCTAAACTCTGCTACTATTTCACCCGACCTACTCGGGAGACC	360

pel.cap	TATTA	ACT	CCTA	TTCTAAC	ACT	CCTAGT	TATT	TTACCCCTGACCTATT	AGGAGACC	360		
gaz.dam	ACT	TTAA	TTCTAG	CCCTCAT	ACT	CCTAGT	CTATT	TCACACCA	GAGATCTGCTTGGAGACC	360		
our.our	TCCT	ACTA	TTCTAG	CCCTCAT	GCTC	CTAGT	CTATT	TCACACCA	GACCTGCTTGGAGACC	360		
ant.cer	ACT	TTAA	TTTAAC	CCCTCAT	GCTC	CTAGT	CTATT	TCACCCGAC	CTGCTTGGAGACC	360		
sai.cat	TA	CTTAA	TTCTAG	CCCTCAT	ACT	CCTAGT	CTATT	TCACCA	GACCTGCTTGGAGACC	360		
mad.kir	TA	CTTAA	TTATAG	CCCTCAT	ACT	CCTAGT	CTATT	TCACCA	GACCTGCTTGGAGACC	360		
rap.mel	TCCT	TTAA	TTAC	CCCTCAT	ACT	CCTAGT	CTATT	CGCACCA	GACCTGCTTGGAGACC	360		
gaz.gaz	TA	CTTAA	TTAC	CCCTCAT	ACT	CCTAGT	CTATT	TCACCCGAC	CTGCTTGGAGACC	360		
ant.ame	TA	CTTAA	TTCTAG	CCCTCAT	ACT	CCTAGT	CTATT	TCACCA	GACCTGCTTGGAGACC	360		
hyd.ine	TCCT	TTAA	TTCTAG	CCCTCAT	ACT	CCTAGT	CTATT	TCACCTGAC	CTGCTTGGAGACC	360		
mun.mun	TA	CTTAA	TTCTAG	CCCTCAT	ACT	CCTAGT	CTATT	TCACCA	GACCTGCTTGGAGACC	360		
alc.alc	TA	CTTAA	TTCTAG	CCCTCAT	ACT	CCTAGT	CTATT	TCACCA	GACCTGCTTGGAGACC	360		
cer.el.a.kan	TA	CTTAA	TTCTAG	ACT	CTTCTTA	A	TAA	TACTAGT	ACTATT	TCACCA	GACCTGCTTGGAGACC	360
cer.el.a.xan	TA	CTTAA	TTCTAG	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACCTGCTTGGAGACC	360
cer.el.a.can	TA	CTTAA	TTCTAG	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACCTGCTTGGAGACC	360
cer.nip.cent	TA	CTTAA	TTCTAG	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACCTGCTTGGAGATC	360
cer.nip.yes	TA	CTTAA	TTCTAG	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACCTGCTTGGAGATC	360
cer.nip.ker	TA	CTTAA	TTCTAG	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACCTGCTTGGAGATC	360
cer.nip.pul	TA	CTTAA	TTCTAG	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACCTGCTTGGAGATC	360
cer.nip.nip	TA	CTTAA	TTCTAG	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACCTGCTTGGAGATC	360
cer.el.a.sco	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACCTGCTTGGAGATC	360
cer.dam	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACCTGCTTGGAGATC	360
ran.tar	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
mos.fus	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
mos.leu	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
mos.chr	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
mos.ber	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
mos.mos	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
tra.jav	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
trag.nap	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
bala.acu	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
bala.bon	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
bala.bor	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
bala.edi	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
esch.reb	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
bala.mus	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
mega.nov	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
bala.phy	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
cap.mar	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
ceph.com	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
ceph.eut	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
lage.obl	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
ceph.hea	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
ceph.hec	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
lage.aus	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
lage.cru	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
lage.obs	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
lisso.boc	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
lisso.pet	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
glo.mac	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
glo.mel	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
fere.att	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
pepo.ele	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
gram.gra	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
pse.cra	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
lage.acu	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
orc.i.bre	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360
orc.a.bre	TA	CTTAA	TTCTGT	ACT	CTTCTTA	A	TAA	TACTAGT	ATT	TCGCACCA	GACTTGTGCTTGGAGACC	360

del.cap	TACTCCTAATCTAACCCCTACTAGCACTGACCCATTCACTCCAGACCTACTAGGAGACC	360
del.tro	TACTCCTAATCTAACCCCTACTAGCACTGACCCATTCACTCCCCGACCTACTAGGAGACC	360
del.del	TACTCCTAATCTAACCCCTACTAGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
sten.cly	TACTCCTAATCTAACCCCTACTAGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
sten.coe	TACTCCTAATCTAACCCCTACTAGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
tur.adu	TACTCCTAATCTAACCCCTACTAGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
sten.fro	TACTCCTAATCTAACCCCTACTAGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
saus.chi	TACTCCTAATCTAACCCCTACTAGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
scen.lon	TACTCCTAATCTAACCCCTACTAGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
turs.tru	TACTCCTAATCTAACCCCTACTAGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
lage.alb	TACTTTAAATCTAACCCCTACTAGCACTAACCCATTCACTCCCCGACCTACTAGGAGATC	360
sten.bre	TACTTTAAATCTAACCTTACTAGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
sota.flu	TACTCCTAATCTAACCCCTACTAGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
del.leu	TACTACTAATCTAACCCCTACTAACGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
mono.mcn	TCATCCTAATCTAACCCCTACTAACGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
plat.gan	TCATCCTAATCTAACCCCTACTAACGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
plat.min	TCATCCTAATCTAACCCCTACTAACGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
kogi.bre	TACTGCTAATCTAACCCCTACTAACGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
kogi.sim	TACTACTAATCTAACCCCTACTAACGCACTAACCCATTCACTCCCCGACCTACTAGGAGATC	360
phys.cat	TACTACTAATCTAACCCCTACTAACGCACTAACCCATTCACTCCCCGACCTACTAGGAGATC	360
lipo.vex	TTCTTATTAATTTGTTCTACTCACACTAACCTTACTTGCAACCGACCTACTGGAGATC	360
phoc.sin	TACTATTAAATCTAACCTTACTAACACTAACCTTACTTGCAACCGACCTACTGGAGACC	360
bera.bai	TACTACTAATCTAACCCCTACTAACGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
ziph.car	TACTATTAAATCGTAATCTACTCGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
meso.eur	TACTACTAATCTAACCCCTACTAACGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
meso.bid	TACTATTAAATCTAACCCCTACTAACGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
meso.den	TACTATTAAATCTAACCCCTACTAACGCACTAACCCATTCACTCCCCGACCTACTAGGAGACC	360
hype.amp	TATTACTNATCTAGTCCTACTCACATTAAACCCATTTCGCACCCGACCTGTAGGAGACC	360
meso.per	TATTATTAAATAGTCCTACTAACCTAACCCATTTCGCACCCGACCTGTAGGAGACC	360
pent.bla	TATTAAATACTCTAACAACTCACGCTGACTCTATTCAACCCCTGACCTACTAGGAGACC	360
hex.lib	TACTTCTTAAATCTAACAACTCACGCTGACTCTATTCAACCCCTGACCTACTAGGAGACC	360
hipp.amp	TACTCCTTAAATCTAACAACTCACGCTGACTCTATTCAACCCCTGACCTACTAGGAGACC	360
dic.sum	TACTTCTTAAATCTAACCCCTACTCACGCTGACTCTATTCAACCCCTGACCTACTAGGAGACC	360
rhin.scn	TGCTTCTTAAATTAGTATTACTCACGCTGACTCTATTCAACCCCTGACCTACTAGGAGACC	360
cera	TACTCCTTAAATCTAACCTACTCACGCTGACTCTATTCAACCCCTGACCTACTAGGAGACC	360
equu	TCTCTCCTAGCTCTACTCTAACCCCTACTTAACTTCAACCCGACCTACTAGGAGACC	360
baby.bab	TACTCATTAATTAACTCTAACCTACTTAACTTCAACCCGACCTACTAGGAGACC	360
phac.afr	TATTCTTAAATCTAACCTACTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
sus.bar	TATTCTTAAATCTAACCTACTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
sus.scr.ewb3	TACTACTTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
lama.gla	TACTACTTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
lama.gua	TACTACTTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
vic.vic	TACTACTTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
cam.bac	TGCTACTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
arc.for	TGCTACTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
arc.gaz	TCTTACTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
eum.jub	TCTTACTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
sal.cal	TCTTACTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
odo.sos	TCTTACTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
pho.fasciata	TACTCCTCATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
pho.gro	TACTCCTCATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
pho.vic	TACTCCTCATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
sys.cri	TACTCCTCATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
hyd.lep	TATTCTTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
lep.wed	TACTCTTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
nic.leo	TACTCTTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
sci.buc	TACTCTTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360
ton.rch	TACTCTTAAATCTAACCTTAACTTCAACCCGACCTACTAGGAGACC	360

hela.mal	TACTTCTTACCCCTAACCCCTAACCAACCCCTACTTGTATTCTGCCCGGACTTACTAGGAGACC	360
sel.thi	TACTTCTCATCCTAGCCCTAGCAACTCTACTGCTTATTCTGCCCGGACTTACTAGGAGACC	360
ail.ful	TACTCTTATCTTAATTCTCATGACATTAGTACTCTACTTCTACCTGACTTGTGTCGTGATC	360
fel	TACTACTGTTAACACTCATACTACTCTGCTTATTTTCACCAGACTCTAGGAGACC	360
can	TACTCTTACTCTAACCTAAATCACTAGTTTATTTCACCTGACTTATTAGGAGACC	360
tal	TAATCTTAATTATAGCTCTATCATCATTAGTATTATTTCACCTGACCTACTAGGAGACC	360
gia.sab	TAATCTCATCTTAATCTCTAACCCCTAGTTCTTCACCCCGATCTTAGGAGACC	360
gia.vol	TAATCTTATCTTAATCTCTAACCCCTAGTTCTTCACCCCGATCTTAGGAGACC	360
byl.pha	TTATTTCTCTCTAACTTTATAAAGTACTACTACTTCTTCTCCCCGATCTTAGGAGACC	360
pes.sec	TTATTTCTCTCTAACTTTATAAAGTACTACTACTTCTTCTCCCCGATCTTAGGAGACC	360
bel.pea	TAATCTTGGCCTTATTTAACCCCTTATTCTATAATCTACTCTCTTACTCCAGACCTCTGGAGACC	360
pce.mcm	TTCTCTTGGCCTTCTTACTTAATCTACTCTCTTACTCTGACTCTGGAGACC	360
Gala.demi	TTATTCCTTACTAACCTCTGTTCTCCCTACTTAATCTCTCCCCGACTTACTAGGAGACC	360
pero.gct	TCTTCTTCTACTAACCTCTACTAACCTACTGCTTACTTCTCCCCGACTTACTAGGAGACC	360
gala.mat	TCTTCTTACTACTATGCCTTACTCTCTACTACTTCTCCCCGACTTACTGGAGACC	360
gala.moh	TCTCTTACTATTATCCCTTACTCTCTACTACTTCTCCCCGACTTACTGGAGACC	360
oco.gaz	TCCTCCCTTCTAACCCCTTCTCTGCTTACTCTGACTTACTAGGAGACC	360
lor.taz	TTGCTCTTAAATCACCTTATCTACTCTACTGCTTACTTCTCCCCGACTTACTAGGAGACC	360
nyc.cou	TTTCCTTATTAGCAACCCCTTCTCTACTCTTACTGCTTACTTCTCCCCGACTTACTAGGAGACC	360
mus	TAATCTTCTTCTAACCTTCTCTACTAACCTACTGCTTACTTCTCCCCGACTTACTAGGAGACC	360
gorz	TCCTCTTCTCTGACCTTCTAACCTAACCTTACTTCTAACCTGACTCTAGGAGACC	360
homo	TTCTCTTCTTCTCTCTTAAATGACATTAAACCTTACTTCTCCCCGACTTACTGGAGACC	360
dug.dug	TCCTCTCATCTCTACTCTTCTACTAACCTGCTTACTCTCTACTCTGAGACTCTAGGAGACC	360
ele.max	TTATCTTATTTTACTCTCTTACTCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
aff.con	CACTCTGCTCTTCTGACCTACTGCTTACTCTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
pavo.mut	CTCTTATTTTACTCTCTGACCTACTGCTTACTCTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
tra.bly	CACTCTGCTCTTCTGACCTACTGCTTACTCTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
tra.sac	CACTCATCTCTTCTGACCTACTGCTTACTCTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
tra.cob	CACTCATCTCTTCTGACCTACTGCTTACTCTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
tra.tem	CACTCATCTCTTCTGACCTACTGCTTACTCTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
arg.arg	CACTCATCTCTTCTGACCTACTGCTTACTCTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
cat.wal	CACTTATTCCTCTTCTGACCTACTGCTTACTCTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
cro.cro	CACTTATTCCTCTTCTGACCTACTGCTTACTCTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
sym.ree	CACTTATTCCTCTTCTGACCTACTGCTTACTCTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
bam.tho	CCCTTATTCCTCTTCTGACCTACTGCTTACTCTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
fra.fra	CACTTATTCCTCTTCTGACCTACTGCTTACTCTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
ith.cru	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
ant.par	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
ant.vir	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
stu.ant.ant	CACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
stu.ant.gil	CACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
stu.ant.sha	CACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
stu.leu	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
stu.can.pra	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
stu.can.sow	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
stu.can.tab	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
stu.can.can	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
stu.ame	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
stu.gru	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
stu.mon	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
stu.nig	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
stu.jap	CACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
cic.boy	CACTCCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
she.ame	CTCTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
ant.alb	CACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
fil.fil	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
fil.vuc	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360
fil.psc	TACTCATCTACTCTTCTGACCTACTGCTTACTCTGCTTACTCTGAGACTCTAGGAGACC	360

fal.spa	TGCTCATACTCCTGCCCTAAAGCCCTAGCCCTATTCAACCCAAACCTGCTAGGAGACC	360
ayt.ame	TCCTCATGCTCACCCCCCTAAATAGCACTAGCCCTATTCTCACCAAACCTCTAGGAGACC	360
smi.sha	CAATCATACTAACACCACTAAATAACCCCTAGCCATATTCTCTCCTAACCTCTAGGAGACC	360
vid.cha	TACTAATATTGGCACTCCTAGCTTCCATAGCCCTATTCTCCCCAACATACTAGGAGATC	360
chry.pic	TTCTAATACTAACCCCTCTACTAACCCCTAACACTATTCTCTCCTAACCTCTAGGAGACC	360
emy.orb.kur	TCCTAATACTAGCCTCTGCTAACCCCTAACACTATTCTCTCCTAACCTCTAGGAGACC	360
che.mud	TTTAATACTAACCTCTCTAACCTAACACTTTCTCCCCCTACTTACTAGGAGACC	360
eum.egr	TCATTATACTGTCTGTTCTACTAGCCCTGCCCTTTCTCACCAAACCTCTAGGCGACC	360

aep.mel	CAGACAANNACATCCCCGAAACCCACTCAACACCCCTCCCCACATCAAGCCCAGAATGGT	420
ore.ore	CAGATAACTACACCCCGAGCAAAACCCACTCAACACTCCCCCTCACATTAAACCGAGAATGGT	420
add.nas	CAGACAATTATAACCCCGAGCAAAACCCACTTAAACACACCCCCCTCACATCAAACCCGAATGGT	420
ory.dam	CAGATAATTATAACACCCAGCAAAACCCACTTAAACACACCCCCCTCACATCAAACCCGAATGGT	420
hip.equ	CAGACAACATGCCCGAGCAAAACCCACTCAACACGGGGCCCTCACATTAAACCCGAATGGT	420
alc.bus	CAGACAACATACACCCCGCGAACCCACTTAAACACACCCCCCTCACATCAAGCCCAGAATGGT	420
sig.lic	CAGACAACATACACCCCGCGAACCCACTTAAACACACCCCCCTCACATCAAGCCCAGAATGGT	420
bea.hun	CAGACAACATACACCCCGCAAAACCCACTTAAATACACCCCCCTCACATCAAACCCGAATGGT	420
dam.lun	CAGACAACATACACCCCTGCIAACCCACTCAACACGGGGCCCTCACATCAAGCCCAGAATGGT	420
con.tau	CAGACAACATACACCCCGCAAAACCCACTCAACACACCCCCCTCACATCAAGCCCAGAATGGT	420
amm.ler	CAGACAACATACACCCAGCAAAACCCACTCAACACACCCCCCTCATATTAAACCTGAATGGT	420
pse.nay	CAGACAACATACACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCCGAGTGT	420
cap.ibe	CAGACAACATACACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCTGAATGGT	420
hem.jem	CAGACAACATACACCCAGCAAAACCCACTCAACACACCCCCCTCATATTCAAACCTGAGTGGT	420
cap.fal	CAGATAACTATACCCAGCAAAACCCACTCAACACACCCCCCTCACATTCAAACCCGAATGGT	420
rup.pyr	CAGATAACTATACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCCGAGTGT	420
rup.rup	CAGATAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCTGAATGGT	420
nem.cau	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCCGAGTGT	420
bud.tax.tax	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCTGAATGGT	420
pan.hod	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCTGAATGGT	420
ovi.amm	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCTGAATGGT	420
ovi.vig	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCTGAATGGT	420
cap.cri	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCCGAGTGT	420
ovi.mos	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCCAGAGTGT	420
ore.ame	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCCGAGTGT	420
cep.dor	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCCGAGTGT	420
cep.max	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCCGAGTGT	420
bis.bon	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCCGAGTGT	420
bos.gru	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCCGAGTGT	420
bos.tra	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCCGAGTGT	420
bub.min	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCCGAGTGT	420
buba.bub	CAGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTAAACCCGAGTGT	420
tra.ang	CCGACAACATACACCCAGCAAAACCCACTCAACACACCCCCCTCATATTCAAACCTGAATGGT	420
tra.eur	CCGACAACATACACCCAGCAAAACCCACTCAACACACCCCCCTCATATTCAAACCTGAATGGT	420
kob.elli	CTGACAACATACACCCAGCAAAACCCACTTAAACACACCCCCCTCACATTAAACCTGAATGGT	420
kob.meg	CTGACAATTATAACCCAGCAAAACCCACTTAAATACACCTCCCCCATATTAAACCCGAATGGT	420
red.aru	CCGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCATATTAAACCCGAATGGT	420
red.ful	CCGACAATTATAACCCAGCAAAACCCACTCAACACACCCCCCTCACATTCAAACCCGAATGGT	420
neo.mos	CAGACAACATACACCCCTCAAAACCCCTTAAACACACCCCCCTCATATTCAAACCCGAATGGT	420
pel.cap	CTGACAATTACACCCCTGCAAAACCGCTCAACACACCCCCCTCATATTCAAACCCGAATGGT	420
gaz.dam	CAGACAACATACACCCAGCAAAACCCACTCAACACACCCCCCATATTAAACCCGAGTGT	420
our.out	CAGACAACATACACCCAGCAAAACCCACTAAATACACCCCCCATATTAAACCCGAGTGT	420
anz.cer	CAGACAACATACACCCAGCAAAACCCACTTAAATACACCCCCCATATTCAAACCCGAATGGT	420
sai.tat	CAGACAACATACACCCAGCAAAACCCACTTAAACACACCCCCCATATTAAACCCGAATGGT	420
mad.kir	CAGACAACATACACCCAGCAAAACCCACTTAAACACACCCCCCATATTCAAACCCGAATGGT	420
rap.mel	CAGACAACATACACCCAGCAAAACCCACTTAAACACACCCCCCATATTCAAACCCGAATGGT	420
gaz.gaz	CAGACAACATACACCCAGCAAAACCCACTTAAACACACCCCCCATATTCAAACCCGAATGGT	420
ant.ame	CCGACAACATACACCCAGCTAACCCACTCAACACACCCCCCATATTAAACCCGAGAATGGT	420

turs.cru	CTGATAACTACACCCCCAGCAAACCCACTAAGCACCCCTGCACACATCAAAACCAGAATGAT	420
lage.alb	CCGATAACTATAACCCAGCAAATCCACTAAGCACCTCTGCACACATCAAAACCAGAATGAT	420
sten.bre	CCGACAACATACCCCCAGCAAATCCACTAAGCACCCCTGCACACATCAAAACCAGAATGAT	420
sota.flu	CCGACAACATACTCCAGCAAATCCACTTAACACCCCTGCACACATCAAAACCAGAATGAT	420
del.leu	CAGACAATTACACCCCCAGCAAACCCACTAAACACCCCCGGCACACATCAAAACCAGAATGAT	420
mono.mon	CTGACAATTATAACCCCCAGCAAACCCACTAAGCACCCCTGCACACATCAAAACCAGAATGAT	420
plat.gan	CCGATAACTACACCCCCAGCAAACCCGTTAATACCCCAGCACATATCAAAACCAGAATGAT	420
plat.min	CCGATAACTACACCCCCAGCAAACCCGTTAATACCCCAGCACATATCAAAACCAGAATGAT	420
kogi.bre	CTGACAACATACCCCCAGCAAACCCACTAAGCACCCGGCACACATTAAACCAGAATGAT	420
kogi.sim	CCGACAACATACCCCCAGCAAACCCACTAAATACCCCACACATATCAAAACCAGAATGAT	420
phys.cat	CTGACAACATACCCCCAGCAAACCCACTAAATCCACTAAACACACATCAAAACCAGAATGAT	420
lipo.vex	CTGACAATTATAACCCCCAGCAAACCCACTAAACACTTCCGACACATTAAACCAGAATGAT	420
phoc.sin	CCGATAACTACATTCCAGCAAACCCACTAAGCACCCAGCACACATTAAAGCCAGAATGAT	420
bera.bai	CCGACAACATACCCCCGGCAAAACCGCTAGCACCCCACACATATTAAAGCCAGAATGAT	420
ziph.car	CCGATAACATACCCCCAGCAAACCCACTTCAGCACCCAGGCACACATCAAAACCAGAATGAT	420
meso.eur	CCGACAATTACACCCCCAGCAAACCCACTTAATACTCCAGCACACATCAAAACCAGAATGAT	420
meso.bid	CCGACAACATACCCCCAGCAAACCCACTTCAGCACCCAGCCACACATCAAAACCAGAATGAT	420
meso.den	CCGACAATTATAACTCCAGCAAACCCACTTCAGCACACATCAAAACCAGAATGAT	420
hyde.amp	CTGACAACATACCCCCAGCAAACCCACTTCAGCACTCCAGCACACATCAAAACCAGAATGAT	420
meso.per	CTGACAATTACACTCCAGCAAACCCACTTAGCACCCAGCACATATTAAACCAGAATGAT	420
pont.bla	CAGACAACATATCCCAGCAAACCCCATGAATAACCCAGAGCATTAAACCAGAATGAT	420
hex.lib	CAGACAACATACCCCCGGCAAACCCCTTAGCACACCACACATCAAAACCAGAATGAT	420
hipp.amp	CAGACAACATACCCCCGGCAAACCCCTTAGCACACCACACATCAAAACCAGAATGAT	420
dic.sum	CGGACAACATACACCCGCCAACCCCTCTCAGCACCCCTCCACACATTAAACCAGAATGAT	420
rhin.son	CAGACAACATACCCCAGCCAACCCCTCTCAGCACCCCTCCACATATCAAAACCAGAATGAT	420
cera	CTGACAACATACCCCCAGCTAACCCCTCTCAGCACTCCCCCTCATATTAAAGCCAGAATGAT	420
equu	CAGACAACATACCCCCAGCTAACCCCTCTCAGCACTCCCCCTCATATTAAAGCCAGAATGAT	420
baby.bab	CGGACAACATACTCCAGCAAACCCACTAAACACACCACCCACATCAAAACCAGAATGAT	420
phac.afr	CAGACAACATACCCCCAGCAAACCCACTAAACACCCACCCCATATTAAACCAGAATGAT	420
sus.bar	CAGACAACATACCCCCAGCAAACCCACTAAACACCCACCCCATATTAAACCAGAATGAT	420
sus.scr.ewb3	CCGACAACATACTCCCCTCAACACACCCCCCCCATTAAACCAGAATGAT	420
lama.gla	CCGACAACATACTCCCCTCAACACACCCCCCTCATATTAAACCAGAATGAT	420
lama.gua	CCGACAACATACCCCCGCTAACCCCTTAACACACCCACCCCATATTAAACCAGAATGAT	420
vic.vic	CTGACAACATACTCCCCTGCTAACCCCTCTCAGCACTCCCCCACATATCAAAACCAGAATGAT	420
cam.bac	CAGACAACATACCCCCAGCCAACCCCTCTCAGCACTCCCCCACATATTAAAGCCGGAAATGAT	420
arc.for	CGGACAATTACACCCCCAGCCAACCCCTCTCAGCACTCCCCCACATATTAAACCTGAATGAT	420
arc.gaz	CCGACAACATACTCCCCTCAACACACCCCCCTCATATTAAACCAGAATGAT	420
eum.jub	CCGACAACATACTCCCCTCAACACACCCCCCACATATTAAACCAGAATGAT	420
tal.cal	CAGACAACATATCCCAGCCAACCCCTCTCAGCACTCCCCCACATATTAAACCTGAATGAT	420
odo.ras	CGGACAATTACACCCCCAGCCAACCCCTCTCAGCACTCCCCCACATATTAAACCTGAATGAT	420
pho.fasciata	CCGACAACATACCCCCCTGCTAACCCCTTAAGCACCCCCACCATATCAAGCCCCGAATGAT	420
pho.gro	CCGACAACATACCCCCTGCTAACCCCTTAAGTACCCCCACCATATCAAGCCCCGAATGAT	420
pho.vit	CCGACAACATATCCCCTGCTAACCCCTTAAGCACCCCCACCATATCAAAACCTGAATGAT	420
cys.cri	CCGACAACATATCCCCTGCTAACCCCTTAAGTACCCCCACCATATTAAACCTGAATGAT	420
hyd.lep	CCGACAACATACTCCCCTGCTAACCCCTTAAGTACTCCACCATATCAAAACCTGAATGAT	420
lep.wed	CCGACAACATACCCCCCTGCTAACCCCTTAAGCACCCCCACCATATTAAACCTGAATGAT	420
mir.leo	CCGACAACATACCCCCCTGCTAACCCCTTAAGCACCCCCACCATATTAAACCTGAATGAT	420
esi.bar	CCGACAACATACTCCCCTGCTAACCCCTTAAGCACCCCCACCATATTAAACCTGAATGAT	420
non.sch	CTGACAACATACCCCCGCAAATCCATTGAGCACCCCCACCATATCAAAACCCTGAATGAT	420
vel.mal	CTGACAACATACCCCCGCAAATCCATTGAGCACCCCCACCATATTAAACCTGAATGAT	420
vel.chi	CTGACAACATACCCCCGCAAATCCATTGAGCACCCCCACCATATTAAACCTGAATGAT	420
til.ful	CTGACAACATATCCCCTGCTAACCCCTTAAGCACCCCCACCATATTAAACCTGAATGAT	420
lei	CAGACAACATACCCCAGCCAACCCCTTTAAATACCCCTCCCCCATATTAAACCTGAATGAT	420
tan	CAGACAACATACCCCCGCAAACCCCTTAACACCCCTCCCCCATATTAAACCTGAATGAT	420
ai	CAGACAATTACATCCCAGCCAACCCCTTAACACCCCTCCCCCATATTAAACCTGAATGAT	420
ta.sib	CAGACAACATACCCCCAGCCAACCCACTTAACACCCCTCCCCCATATTAAACCTGAATGAT	420
ta.vol	CAGACAACATACTCCAGCCAACCCACTTAACACCCCTCCCCCATATTAAACCTGAATGAT	420
yl.phu	CTGACAACATACCCCCGGCAAACCCACTTAACACCCCTCCCCCATATTAAACCTGAATGAT	420

aep.mel	ACTTCCTGTTNGCATACGCAATCCTACGGATCAATCCCCAATAAACTAGGGAGG	472
ore.ore	ATTTCTATTNGCATATGCCAATCCTACGGATCAATCCCCAATAAACTAGGGAGG	472
add.nas	ATTTCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
ory.dam	ATTTCTATTNGCATATGCCATCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
hip.equ	ATTTCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
alc.bus	ATTTCTATTNGCATATGCCATCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
sig.lic	ATTTCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
bea.hun	ATTTCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
dam.lun	ATTTCTATTNGCATACGCAATTCTACGGATCAATCCCCAACGGAGCTAGGGAGG	472
con.tau	ACTTCCTATTNGCATATGCCAATCCTACGGATCAATCCCCAACGGACTAGGGAGG	472
amm.ler	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAGCTAGGGAGG	472
pse.nay	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGGGG	472
cap.ibe	ATTTCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
hem.jem	ATTTCTATTNGCATACGCGATCCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
cap.fal	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTGGGAGG	472
rup.pyr	ATTTCTTGTGTTGCATATGCCATCTACGGATCAATCCCCAACAAAACCTGGGAGG	472
rup.rup	ATTTCTTATTNGCATATGCCATCTACGGATCAATCCCCAACAAAACCTGGGAGG	472
nem.cau	ATTTCTATTNGCATATGCCAATCTTACGGATCAATCCCCAACAAAACCTAGGGGG	472
bud.tax.tax	ATTTCTATTNGCATATGCCAATCTTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
pan.hod	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
ovi.amm	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
ovi.vig	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
cap.cri	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
ovi.mos	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
ore.ame	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
cep.dor	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
cep.max	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
bis.bon	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
bos.gru	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
bos.tra	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
bub.min	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
buba.bub	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
tra.ang	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
tra.eur	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
kob.ell	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
kob.meg	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
red.aru	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
red.ful	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
neo.mos	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
pel.cap	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
gaz.dam	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
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ant.cer	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
sai.cat	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
mad.kir	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
cap.mel	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
gaz.gaz	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
anc.ame	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
hyd.ine	ACTTCCTATTNGCATACGCAATTCTACGGATCAATCCCCAACAAAACCTAGGGAGG	472
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cer.elo.sco	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAACTAGGAGG 472
cer.dam	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAATAAAATTAGGAGG 472
ran.tar	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAATAAAACTAGGAGG 472
mos.fus	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAACTAGGAGG 472
mos.leu	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAACTAGGAGG 472
mos.chr	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAACTAGGAGG 472
mos.ber	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAACTAGGAGG 472
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era.jav	ATTTCTATTGCAATCGCAATTCTCGGTCAATTCCAAATAAAATTAGGAGG 472
trag.nap	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAATAAAATTAGGAGG 472
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bala.bor	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
bala.edi	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
esch.rob	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
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ceph.com	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAATAAAACTTTGGAGG 472
ceph.eut	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAATAAAACTTTGGAGG 472
lage.obl	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
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ceph.hec	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
lage.aus	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
lage.cru	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
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glo.mel	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
fere.att	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
pepo.ele	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
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sten.fro	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
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sten.lan	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
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lage.alb	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
sten.bre	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
sota.flu	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
del.leu	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
mono.mon	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
plac.gan	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
plac.min	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472
kogi.bce	ATTTCTATTGCAATCGCAATCCTACGATCAATTCCAAACAAATTAGGCGG 472

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cer.nip.nip	CAGACAACTACACCCCCAGCAAACCCACTCAACACACACCCCCCTCATATTAAACCTGAATGAT	420
cer.elo.sco	CAGACAAATTACACTCCAGCAAATCCACTCAACACACACCTCTCATATTAAACCGAATGAT	420
cer.dam	CAGACAACTATAACCCAGCAAACCCACTCAACACTCCCCCTCATATTAAACCTGAATGAT	420
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mos.fus	CGGACAAATTATAACCCAGCAAACCCATTAAATACACCCCCCACATATTAAACCCGAATGAT	420
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tra.jav	CAGATAACTACACCCCCGGCAAACCCCTTAACACACACCCCCCTATCAAACCCGAATGAT	420
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mega.nov	CAGACAACTATAACCCAGCAAACCCACTCACTCACTACCCAGGCACACATTAAACCGAATGGT	420
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tur.adu	CTGACAACTATAACCCAGCAAATCCATTAAAGCACCCCCGGCACACATCAAACCCAGAGGT	420
sten.fro	CTGACAACTATAACCCAGCAAATCCATTAAAGCACCCCCGGCACACATCAAACCCAGAGGT	420
caus.chi	CCGACAACTATAACCCAGCAAATCCATTAAAGCACCCCCGGCACACATCAAACCCAGAGGT	420
sten.lon	CTGACAACTATAACCCAGCAAATCCATTAAAGCACCCCCGGCACACATCAAACCCAGAGGT	420

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 mus ATTTCTATTGGCATACGCCATTCTACGCTCAAATCCCCAATAAAACTAGGAGG 472
 gorr ATTTCTATTGGCTACGCCATTCTCCGATCTGTCCCCAATAAAACTAGGAGG 472
 homo ATTTCTATTGGCTACACAATTCTCCGATCCGTCCCTAACAAACTAGGAGG 472
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 afr.con ATTTCTATTGGCTACGCCATTCTCGCTCAAATCCCCAACAAACTAGGAGG 472
 pavo.muc ACTTCTATTGGCTACGCCATTCTCGCTCAAATCCCCAACAAACTAGGAGG 472
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 smi.sha ATTTCTATTGGCTTACGCCATTCTACGCTCAAATCCCCAACAAACTAGGAGG 472
 vid.cha ATTTCTATTGGCTTACGCCATTCTACGCTCAAATCCCCAACAAACTAGGAGG 472
 chry.pic ATTTCTTTTGCTTACGCCATTCTACGCTCAAATCCCCAACAAACTAGGAGG 472
 emy.orb.kur ATTTCTTTTGCTTACGCCATTCTACGCTCAAATCCCCAACAAACTAGGAGG 472
 che.mud ATTTCTATTGGCTTACGCCATTCTACGCTCAAATCCCCAACAAACTAGGAGG 472
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 PRIMER 'mcb863' CGATCAAATCCCCTAACAAACTAGGAGG
 * * * * *

Results for RID 984593689-1224-27770



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593689-1224-27770

Query=

(328 letters)

Database: Sequences from complete mitochondrial genomes
129 sequences; 3,164,247 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQs

Taxonomic reportsDistribution of 80 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

			(bits)	Value
<u>ref NC_001700_1 </u>	Felis catus mitochondrion, complete genome	365	e-101	
<u>ref NC_001325_1 </u>	Phoca vitulina mitochondrion, complete genome	198	1e-51	
<u>ref NC_002008_1 </u>	Canis familiaris mitochondrion, complete g...	190	4e-49	
<u>ref NC_001602_1 </u>	Halichoerus grypus mitochondrion, complete...	180	3e-46	
<u>ref NC_000884_1 </u>	Cavia porcellus complete mitochondrial genome	176	5e-45	
<u>ref NC_001808_1 </u>	Ceratotherium simum mitochondrion, complet...	155	2e-41	
<u>ref NC_001892_1 </u>	Myoxus glis mitochondrion, complete genome	153	8e-38	
<u>ref NC_001788_1 </u>	Equus asinus mitochondrion, complete genome	151	3e-37	
<u>ref NC_002073_1 </u>	Orycteropus afer complete mitochondrial ge...	149	1e-36	
<u>ref NC_001821_1 </u>	Dasyurus novemcinctus mitochondrion, comple...	141	3e-34	
<u>ref NC_001779_1 </u>	R.unicornis complete mitochondrial genome	135	2e-32	
<u>ref NC_001569_1 </u>	Mus musculus mitochondrion, complete genome	133	7e-32	
<u>ref NC_000889_1 </u>	Hippopotamus amphibius mitochondrion, comp...	125	2e-29	
<u>ref NC_001640_1 </u>	Equus caballus mitochondrion, complete genome	125	2e-29	
<u>ref NC_001794_1 </u>	Macropus robustus mitochondrion, complete ...	123	7e-29	
<u>ref NC_000845_1 </u>	Sus scrofa mitochondrion, complete genome	121	3e-28	
<u>ref NC_001665_1 </u>	Rattus norvegicus mitochondrial genome	121	3e-28	
<u>ref NC_001567_1 </u>	Bos taurus mitochondrion, complete genome	121	3e-28	
<u>ref NC_001643_1 </u>	Pan troglodytes mitochondrion, complete ge...	117	4e-27	
<u>ref NC_001941_1 </u>	Ovis aries mitochondrion, complete genome	109	1e-24	
<u>ref NC_002391_1 </u>	Talpa europaea mitochondrion, complete genome	103	7e-23	
<u>ref NC_001913_1 </u>	Oryctolagus cuniculus mitochondrion, compl...	103	7e-23	
<u>ref NC_001644_1 </u>	Pan paniscus mitochondrion, complete genome	101	3e-22	
<u>ref NC_001807_2 </u>	Human mitochondrion, complete genome	98	4e-21	
<u>ref NC_001601_1 </u>	Balaenoptera physalus mitochondrion, compl...	98	4e-21	
<u>ref NC_002009_1 </u>	Artibeus jamaicensis mitochondrion, comple...	96	2e-20	
<u>ref NC_001645_1 </u>	Gorilla gorilla mitochondrion, complete ge...	92	2e-19	
<u>ref NC_001321_1 </u>	Balaenoptera acutorostrata mitochondrion, compl...	90	1e-18	
<u>ref NC_001610_1 </u>	Didelphis virginiana mitochondrion, comple...	80	9e-16	
<u>ref NC_002082_1 </u>	Hylobates lar mitochondrion, complete genome	70	9e-13	
<u>ref NC_001727_1 </u>	Crossostoma lacustre mitochondrion, comple...	70	9e-13	
<u>ref NC_001804_1 </u>	Latimeria chalumnae mitochondrion, complet...	68	4e-12	
<u>ref NC_000880_1 </u>	Vidua chalybeata mitochondrion, complete g...	66	1e-11	
<u>ref NC_002069_1 </u>	Corvus frugilegus mitochondrion, complete ...	64	6e-11	
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<u>ref NC_001646_1 </u>	Pongo pygmaeus mitochondrion, complete genome	62	2e-10	
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<u>ref NC_000890_1 </u>	Mustelus manazo mitochondrion, complete ge...	60	9e-10	
<u>ref NC_001323_1 </u>	Gallus gallus mitochondrion, complete genome	60	9e-10	
<u>ref NC_002079_1 </u>	Carassius auratus mitochondrion, complete ...	58	3e-09	
<u>ref NC_000934_1 </u>	Loxodonta africana mitochondrion, complete...	56	1e-08	
<u>ref NC_000878_1 </u>	Falco peregrinus mitochondrion, complete g...	56	1e-08	
<u>ref NC_000846_1 </u>	Rhea americana mitochondrion, complete genome	54	5e-08	
<u>ref NC_002196_1 </u>	Ciconia boyciana mitochondrion, complete g...	54	5e-08	
<u>ref NC_001960_1 </u>	Salmo salar mitochondrion, complete genome	54	5e-08	
<u>ref NC_001788_1 </u>	Polypterus ornatipinnis mitochondrion, com...	52	2e-07	
<u>ref NC_002083_1 </u>	Pongo pygmaeus abelii mitochondrion, compl...	52	2e-07	
<u>ref NC_001953_1 </u>	Struthio camelus complete mitochondrial ge...	52	2e-07	
<u>ref NC_001947_1 </u>	Pelomedusa subrufa mitochondrion, complete...	52	2e-07	
<u>ref NC_001770_1 </u>	Arbacia lixula mitochondrion, complete genome	52	2e-07	

Alignments

tmpseq_0	1	tgaatctggaggaggcttcaggtagacaaagctaccctgacacgattttgccttccac	60
NC_001700	15524g...g.....c....d.....g.....	15583
NC_001325	15580a..t.....t....a..t.a.....c.....	15639
NC_002008	14673	c.....g.....a.....a.....a.....	14729
NC_001602	15553a..t.....a..t.a...g.....c.....	15612
NC_000884	14650	g...g.....c.....a.....	14709
NC_001808	14662a..t.c..t.....c..a..t.....c.....t..	14721
NC_001892	14654	c.....c.....t..a..c.....t..a..t..	14713
NC_001788	14671t..a.....c.....c.....c.....	14710
NC_002078	14663c.....t.....c.....a..a..a.....c.....	14716
NC_001921	14557a..t.a..c.....c.....c.....	14723
NC_001779	14664g.....c.....c.....c.....c.....	14684
NC_001562	14625t.....g.....c.....t.....c.....	14717
NC_000892	14658t..c.....c.....t.....	14711
NC_001640	14674t..a.....c.....t..c.....c.....t.....	14727
NC_001724	14670g.....c.....c.....c.....c.....c.....	14727

NC_000845	15828g....t..c..c.....a....c.....c.....c.....a.....14669
NC_001665	14610a.....a....c.....c.....c.....c.....a.....15059
NC_001567	15000c.a.....a....t..c.....c.....c.....c.....ca.....14710
NC_001643	14655a.....gcc.....t.....c.....c.....c.....t...14704
NC_001941	14645g....a.....c.....c.....c.....c.....c.....14730
NC_002191	14671t....c..g.....g..a..c.....c.....c.....c.....14720
NC_001913	14661a.t....t..t.....c..t..t..c.....c.....c.....14711
NC_001644	14656a.....gcc.....t.....c.....c.....a....t...15292
NC_001807	15233a.....gtc.c..c.....c.....a....t.....15155
NC_001601	15096c..t..t..t..s..t....a..a..a..c.....c.....t.....14695
NC_002009	14636t....c.....a..t..c..c.....c.....c.....a.....14714
NC_001645	14686a.....c.....c.....t.....a..a..a..c.....t.....15158
NC_001321	15099c..c.....t.....t....a..a..a..c.....t.....t...14722
NC_001610	14663t....a..c..t..c.....a..a..c.....t.....t.....14712
NC_002082	14657c..a.....t..c..c..a..c.....c..t..ca.....t...15823
NC_001737	15764s..g.....t..a..t.....g.....c.....14888
NC_001804	14829t..t..c.....c..c..a..c..s.....15500
NC_000880	15477a.....cc..c..a..a..c.....14243
NC_002069	14190t..a.....t.....ca.....14777
NC_000886	14719g..t.....t..a....a..c.....ca.....14736
NC_001646	14716a.....a.....a..c.....15838
NC_001606	15779t..g.....t..a..a..a.....c..a.....14900
NC_000890	14841s..t.....c..c.....t.....c..t.....15841
NC_002079	15782t.....c..t..t..a..at..a.....t..c..c.....14692
NC_000934	14633t.....t..a..t..a..at..t..c..c.....14263
NC_000878	14222cc..a..a.....c.....c..c..a..14186
NC_000845	14145cc.....a..c.....c..c..s...15929
NC_001950	15870t.....a..t..t.....c.....a.....14822
NC_001778	14763g..t.....t..t..c..a..a..t..c.....c..t...14169
NC_001953	14115c..a.....t.....cc..c.....a.....14854
NC_001947	14805a..t.....t..a..a..c.....15119
NC_001770	15069t.....t.....a..a..c.....t..t...120
tmpseq_0	61	tccatccattatcatccagcttcaggcagccacccatccatccacagag
NC_001700	15584t.....c..t.....ct.....g..a.....t.....t..a.....15643
NC_001325	15640a.....cg..ag..a..t..a..a..ac.....a.....a.....15699
NC_002008	14730c..t..c.....s.....at..a.....t..a.....a.....14789
NC_001502	15613a.....cg..ag..a..t..a.....a.....a.....a.....15672
NC_000884	14710t.....c.....a..c..c.....tgat.....t.....c.....14769
NC_001808	14722t.....c..c.....t..ac..c.....atcac.....a.....14781
NC_001892	14714t..a..c..c..t..tg.....c..t..at.....t.....c.....14773
NC_001788	14731t..a..c.....a..c..g..t..atc.....t..a.....c.....14790
NC_002078	14717t.....g.....t..tg.....tat.....t..a.....t..a.....14776
NC_001821	14717t..a.....t..a..a..c..t..t.....gt.....a.....a.....14776
NC_001779	14724t.....c..c..t..ct..c.....a..c.....a.....a.....a.....14783
		c
NC_001569	14685t..a.....t..g..g..c.....atc..t.....c.....c.....a.....14744
NC_000889	14718t..c.....cg..t..a..a..a..atc.....t..a.....c..t..a.....14777
NC_001630	14734a..c..c.....a..c..g..t..tc..a..t..a.....t.....a.....14793
NC_001794	14730t..a.....a..c..t..ct..t.....a.....14789
NC_001794	1446214475
NC_000845	15888t.....g.....c.....ta..c..c..c.....a..t.....g.....a.....15947
NC_001665	14670c.....c..t..s..g..c..c..t..act..a..t..t..c.....c.....14729
NC_001567	15060t.....at..aa..t..cat.....a.....c.....15119
NC_001643	14711t..t..a..c..c.....a..a..a..c..t.....t.....c..a.....14770
NC_001941	14705t..tt..c.....c.....g..c..c..cat..t.....a..c.....c.....14764
NC_002191	14731t..g.....t..tg..s..a.....t..g..t.....gt.....t.....14790
NC_001913	14721t..g.....14740
NC_001644	14712t..a..c..c..t..a..c..a..a..c..t..t.....t..a.....a.....14771
NC_001807	15293t..g..c..c..t..tg.....a..c.....t..g.....a.....15352
NC_001601	15156t..c..c..c.....tat..at.....atc.....a..c.....15215
NC_002009	14595cc..a.....c..c..tg..aa.....t..at.....cc.....t..a.....14755
NC_001645	14715t..a..c..c.....a..a..c..a..s..cc.....t.....t..a.....14774
NC_001721	15159t..c..c..c.....ct..at.....atc.....t..at.....t.....14782
NC_001610	14723t..c..c.....c..t..a..t..c..a..t..c..t.....t.....14772
NC_001063	14713a..t..c..t..a..g..c.....cc..g.....t.....a.....15826
NC_001777	1582415843
NC_001737	1587214792
NC_001904	14889c.....g.....14792

<u>NC_001804</u>	14928g..c.....t... 14948
<u>NC_000880</u>	15567ac.....a....a 15591
<u>NC_002069</u>	14244c....a...c...g.a...g...gc...a..ct...t...aacc.....a 14303
<u>NC_000886</u>	14778 14780
<u>NC_001646</u>	14737a..a..t..c.....ta.....a..a.cc.t.....a 14796
<u>NC_001606</u>	15839 15841
<u>NC_000890</u>	14901	... 14902
<u>NC_003079</u>	15842	...c....a..... 15862
<u>NC_000934</u>	14693c..... 14708
<u>NC_000878</u>	14264	...c.a..... 14246
<u>NC_000846</u>	14235 14189
<u>NC_000846</u>	14187	... 15932
<u>NC_001960</u>	15930	... 14833
<u>NC_001778</u>	14823t..... 14184
<u>NC_001953</u>	14170	...c....c..... 15122
<u>NC_001770</u>	15120	... 180
<u>tmpseq_0</u>	121	acaggatctaacaacccctcaggaatacgatccgactcagacaaaattccacctccaccca 15703
<u>NC_001700</u>	15644tac.....t.....c..... 15759
<u>NC_001325</u>	15700a.....c.....ca.....c.....c..... 14849
<u>NC_002008</u>	14790	..c.....c.....c.....cac..a.....c.....t.....t 15732
<u>NC_001602</u>	15673a.....c.....ca..c.....c.....c..... 14829
<u>NC_000884</u>	14770a.....a.....c..aac..a..c.....c.....c..... 14841
<u>NC_001808</u>	14782c..t.....a.....ccc..a..at.....c.....c..... 14833
<u>NC_001892</u>	14774g..t.....a.....t..aac..a..a.....c.....c..... 14850
<u>NC_001788</u>	14791c.....ccc..t..at.....c.....c..... 14836
<u>NC_002078</u>	14777t..t..a..t..t.....c..t.....t..... 14836
<u>NC_001821</u>	14777a.....a..t..cccg..aa..at.....c..c..... 14843
<u>NC_001779</u>	14784g..c.....a.....tcc..a..at.....c.....c..... 14804
<u>NC_001569</u>	14745a.....aa..t..aac..a..tg..t.....t.....c..... 14837
<u>NC_000889</u>	14778c.....aa.....cccc..aa..g.....c.....c..... 14853
<u>NC_001640</u>	14794t.....ccc.....tag.....c.....c..... 14849
<u>NC_001794</u>	14790	..c..t.....a..t..caacc.....c.....c..... 16007
<u>NC_000845</u>	15948	..c.....c.....ta.c..ctc..a..at.....t..... 14789
<u>NC_001665</u>	14730a..t.....a..t..aac.....g.....c.....c..... 15179
<u>NC_001567</u>	15120c..c.....aa.....tccc..a..gt.....c.....c..... 14830
<u>NC_001643</u>	14771a..t.....c.....cacc..c..c.....a..c.....c..... 14824
<u>NC_001941</u>	14765c.....a.....tcc..g..a..t.....c.....c..... 14814
<u>NC_003391</u>	14791a.....a..... 14840
<u>NC_001913</u>	14815t.....c..t.....c.....c..... 14831
<u>NC_001644</u>	14772a..t.....ct.....cacc..c..c.....a..c.....c..... 15412
<u>NC_001807</u>	15353	...g.....a.....ct.....cacc..c..t..c.....ca..c..... 15275
<u>NC_001601</u>	15216c.....a..t..ccc..t..at..t..... 14815
<u>NC_002009</u>	14756a.....c..tcc..a..c.....t..... 14834
<u>NC_001545</u>	14775a.....tct..c..cccc..c.....t.....ca..c.....c..... 15278
<u>NC_001321</u>	15219c.....a..c..ccc.....at..t.....c.....c..... 14842
<u>NC_001510</u>	14783a..g..t..aa..cc.....a.....t..... 1
		a.
<u>NC_003082</u>	14773a.....t....c..c..ctcc..c..ac.....cg..c.....c 14832
<u>NC_001727</u>	15884c..c.....g..cc..aac.....g..t....ct..c..... 15943
<u>NC_001804</u>	14949c..... 14965
<u>NC_000880</u>	15592a.....t..aac.....tcc..a..gt..... 15651
<u>NC_002069</u>	14304c..a.....gt..t..tccc..a..gc.....c..... 14363
<u>NC_001645</u>	14797a..t..... 14814
<u>NC_001231</u>	15531t.....t.....c..... 15561
<u>NC_002079</u>	15939t.....t.....c..... 15961
<u>NC_000934</u>	14786c..c..c..... 14812
<u>NC_000879</u>	14363c..... 14383
<u>NC_000845</u>	14247	..c..g..c.....c.....c.....cc..t.....c.....c..... 14306
<u>NC_002195</u>	16171 16391
<u>NC_002081</u>	14858 14866
<u>NC_001951</u>	14269c..c..... 14289
<u>tmpseq_0</u>	181	cactacacaaatcaggatcaccggggccccctcgactatccatcgaccatccatcc 15763
<u>NC_001700</u>	15704c.....c.....a..t.....g..tt..a..... 15817
<u>NC_001325</u>	15760c.....c.....a..ggcc..c..t..c.....cc..a..c..... 14972
<u>NC_002079</u>	14850t..... 15755
<u>NC_001602</u>	15733c..t..... 15772
<u>NC_001590</u>	15706 15772

<u>NC_000884</u>	14830	..t.....	14846
<u>NC_001808</u>	14842c.....aa..t..c.c.....ac.cgcc..a	14901
<u>NC_001892</u>	14834	..t.....t.....c..a....a..cc...c..tt.tccc....acc..a	14893
<u>NC_001788</u>	14851t.....c....a..a....	14882
<u>NC_001788</u>	15080	15095
<u>NC_002078</u>	14837	14853
<u>NC_001821</u>	14837t.....t.....	14859
<u>NC_001779</u>	14844c.....	14866
<u>NC_001569</u>	14805c.....	14827
<u>NC_000889</u>	14838	..t.....g..c.....	14860
<u>NC_001640</u>	14854	..t..t....t....c.....	14876
<u>NC_001640</u>	15085	15098
<u>NC_001794</u>	14850	..t..t..t.....	14867
<u>NC_000845</u>	16008t..t.....	16024
<u>NC_001665</u>	14790	..t..t....t.....	14806
<u>NC_001567</u>	15180t..c..t..g..c....c....t....t..a.....a	15239

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<u>NC_001643</u>	14831	14853
<u>NC_001941</u>	14825	..t....c..t....c.....	14847
<u>NC_001913</u>	14841	14857
<u>NC_001544</u>	14832c.....	14854
<u>NC_001807</u>	15413	15429
<u>NC_001501</u>	15276t.....	15292
<u>NC_002009</u>	14816t..t..t.....	14835
<u>NC_001645</u>	14835c....a.....	14863
<u>NC_001321</u>	15279	...c.....t.....	15295
<u>NC_001610</u>	14843t..c..a.....	14865
<u>NC_002082</u>	14833t.....c.....	14855
<u>NC_001727</u>	15944	15947
<u>NC_000880</u>	15652	15659
<u>NC_002069</u>	14364t.....	14381
<u>NC_001323</u>	15562t.ct....c..t.....	15588
<u>NC_002079</u>	15962	15965
<u>NC_000934</u>	14813	14817
<u>NC_000878</u>	14384t.tc.....	14406
<u>NC_000846</u>	14307	14310
<u>NC_002196</u>	16392t..t.cc.....a.....	16421
<u>NC_002083</u>	14867c....a.....	14895
<u>NC_001953</u>	14290	14293

<u>tmpseq_0</u>	241	gttcatttttttaccagaccgttaggagacccggataactacatccccggccaaacctttta	300
<u>NC_001700</u>	15764t.....c.....a..c.....a.....t..	15823
<u>NC_001325</u>	15820	..g.....c.....a..c.....a..c.....t.....	15867
<u>NC_002008</u>	14914t.....t.....a.....a.....c.....a.....c..	14969
<u>NC_001602</u>	15793	..a.....c.....a..g.....c.....t..c.....	15852
<u>NC_000884</u>	14900c.....a.....a.....ca..c.....g..g	14949
<u>NC_001808</u>	14902	..t.....a.cc.....t..c.....c.....t.....	14960
<u>NC_001892</u>	14894t.....c.....t..a.....c.....c.....a..	14953
<u>NC_002078</u>	14909a.....	14928
<u>NC_000845</u>	16071ac.....a..c.....c..a..a.....a..	16127
<u>NC_001567</u>	15240	..a.....g.....c..cc..c.....a.....c..a....	15232
<u>NC_001913</u>	14901t.....a.....a..c.....c.....c..t..	14950
<u>NC_001644</u>	1484	1492
<u>NC_001807</u>	15476cc..c.....a..c..t..t..c..ta.....cc..	15532
<u>NC_002009</u>	14880t.....cc.....a..c..t..t..t..a..a..c..t	14935
<u>NC_001645</u>	14898cc.....a..c.....c..tta.....c..	14954
<u>NC_001610</u>	14907t..t.....t..c..t..c..a..t..t..c..t	14962
<u>NC_002082</u>	14950	14952
<u>NC_001804</u>	15071a..c...a.....a....	15108
<u>NC_000886</u>	14980a..c...t..c..a.....a.....	15017
<u>NC_002196</u>	16454ca....ac....t....a..g....t..c..a.....	16507
<u>NC_001953</u>	16155c...c..	16169

<u>tmpseq_0</u>	301	atcacccctccatccaaaggctgtatc	328
<u>NC_001700</u>	15824t..a.....	15851
<u>NC_002009</u>	14970	..c.....a..t..a.....	14775
<u>NC_001602</u>	15853	..gc.....a..a.....	15873
<u>NC_000884</u>	14950	14754
<u>NC_001913</u>	14754	..g.....	14770

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<u>NC_001779</u>	<u>3081</u>	3094
<u>NC_000845</u>	<u>16128</u>	..c.....a.....	16144
<u>NC_001911</u>	<u>14961</u>	14980
<u>NC_001644</u>	<u>1493</u>	...c.....	1501
<u>NC_001807</u>	<u>15533</u>	..c.....c.....c....	15560
<u>NC_002009</u>	<u>14936</u>c.....a....	14963
<u>NC_001645</u>	<u>14955</u>	.gc.....a.....c.....	14974
<u>NC_001610</u>	<u>14963</u>	..c.....g..c.....a....	14990
<u>NC_002082</u>	<u>14953</u>	..c.....c.....	14972
<u>NC_001960</u>	<u>16170</u>	gt...t..a..t.....	16197
<u>NC_001951</u>	<u>14416</u>c....	14437

Database: Sequences from complete mitochondrial genomes

Posted date: Jun 28, 2000 10:56 AM

Number of letters in database: 3,164,247

Number of sequences in database: 129

Lambda K H
1.37 0.711 1.31

Gapped
Lambda K H
1.37 0.711 1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 788
Number of Sequences: 129
Number of extensions: 788
Number of successful extensions: 168
Number of sequences better than 10.0: 77
length of query: 328
length of database: 3,164,247
effective HSP length: 15
effective length of query: 313
effective length of database: 3,162,312
effective search space: 989803656
effective search space used: 989803656
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 14 (28.2 bits)

Table 4

BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593400-28182-3122

Query= (328 letters)

Database: nt
807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQs

Taxonomy reportsDistribution of 50 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

		Score (bits)	E Value
Sequences producing significant alignments:			
gb AY005809.1	Panthera pardus cytochrome b gene, partial c...	601	e-170
gb AF053054.1 AF053054	Panthera tigris sumatrae isolate Sul...	527	e-147
gb AF053053.1 AF053053	Panthera tigris tigris isolate 87 mi...	527	e-147
gb AF053050.1 AF053050	Panthera tigris corbetti isolate C2 ...	476	e-132
gb AF053049.1 AF053049	Panthera tigris corbetti isolate Cl ...	476	e-132
gb AF053025.1 AF053025	Panthera tigris tigris isolate B9 cy...	450	e-127
gb AF053024.1 AF053024	Panthera tigris tigris isolate B8 cy...	450	e-127
gb AF053023.1 AF053023	Panthera tigris tigris isolate B7 cy...	450	e-127
gb AF053022.1 AF053022	Panthera tigris tigris isolate B6 cy...	450	e-127
gb AF053021.1 AF053021	Panthera tigris tigris isolate B5 cy...	450	e-127
gb AF053018.1 AF053018	Panthera tigris tigris isolate B2 cy...	452	e-125
gb AF053051.1 AF053051	Panthera tigris corbetti isolate C3 ...	452	e-125
gb AF053048.1 AF053048	Panthera tigris sumatrae isolate Sul...	452	e-125
gb AF053047.1 AF053047	Panthera tigris sumatrae isolate Su9...	452	e-125
gb AF053046.1 AF053046	Panthera tigris sumatrae isolate Su7...	452	e-125
gb AF053045.1 AF053045	Panthera tigris sumatrae isolate Su6...	452	e-125
gb AF053044.1 AF053044	Panthera tigris sumatrae isolate Su5...	452	e-125
gb AF053042.1 AF053042	Panthera tigris sumatrae isolate Su3...	452	e-125
gb AF053041.1 AF053041	Panthera tigris sumatrae isolate Su2...	452	e-125
gb AF053040.1 AF053040	Panthera tigris sumatrae isolate Sul...	452	e-125
gb AF053039.1 AF053039	Panthera tigris altaica isolate S15 ...	452	e-125
gb AF053038.1 AF053038	Panthera tigris altaica isolate S14 ...	452	e-125
gb AF053037.1 AF053037	Panthera tigris altaica isolate S13 ...	452	e-125
gb AF053036.1 AF053036	Panthera tigris altaica isolate S12 ...	452	e-125
gb AF053035.1 AF053035	Panthera tigris altaica isolate S11 ...	452	e-125
gb AF053034.1 AF053034	Panthera tigris altaica isolate S10 ...	452	e-125
gb AF053033.1 AF053033	Panthera tigris altaica isolate S8 c...	452	e-125
gb AF053032.1 AF053032	Panthera tigris altaica isolate S7 c...	452	e-125
gb AF053031.1 AF053031	Panthera tigris altaica isolate S6 c...	452	e-125
gb AF053030.1 AF053030	Panthera tigris altaica isolate S5 c...	452	e-125
gb AF053029.1 AF053029	Panthera tigris altaica isolate S4 c...	452	e-125
gb AF053028.1 AF053028	Panthera tigris altaica isolate S3 c...	452	e-125
gb AF053027.1 AF053027	Panthera tigris altaica isolate S2 c...	452	e-125
gb AF053026.1 AF053026	Panthera tigris tigris isolate B4 cy...	452	e-125
gb AF053020.1 AF053020	Panthera tigris tigris isolate B3 cy...	452	e-125
gb AF053019.1 AF053019	Panthera tigris sumatrae isolate Su4...	444	e-122
emb X82301.1 MIPLCYTB	P.tigris mitochondrial cytochrome b gene	444	e-122
gb AF053052.1 AF053052	Panthera leo cytochrome b (cytb) gen...	440	e-121
emb X82300.1 MIPLCYTB	P.leo mitochondrial cytochrome b gene	438	e-106
dbj AB004238.1 AB004238	Felis catus mitochondrial DNA for c...	399	e-103
dbj AB004237.1 AB004237	Felis catus mitochondrial DNA for c...	381	e-102
emb X82296.1 MIFDCYTB	F.domesticus mitochondrial cytochrome...	377	e-102
ref NC_001700.1	Felis catus mitochondrion, complete genome	365	1e-98
gb U20753.1 FCU20753	Felis catus mitochondrion, complete ge...	355	1e-98
gb AF125145.1 AF125145	Viverricula indica cytochrome b gene...	276	7e-72
gb AF125144.1 AF125144	Chrotogale owstoni cytochrome b gene...	270	4e-70
gb AF154975.1 AF154975	Martes martes specimen_voucher AF175...	255	7e-66
dbj AB051237.1 AB051237	Martes martes mitochondrial cytb ge...	256	7e-66
gb AF125149.1 AF125149	Viverra tangalunga cytochrome b gene...	246	6e-63

Alignments

<u>AF053046</u>	487g..t.....	546
<u>AF053045</u>	487g..t.....	546
<u>AF053044</u>	487g..t.....	546
<u>AF053042</u>	487g..t.....	546
<u>AF053041</u>	487g..t.....	546
<u>AF053040</u>	487g..t.....	546
<u>AF053039</u>	487g..t.....	546
<u>AF053038</u>	487g..t.....	546
<u>AF053037</u>	487g..t.....	546
<u>AF053036</u>	487g..t.....	546
<u>AF053035</u>	487g..t.....	546
<u>AF053034</u>	487g..t.....	546
<u>AF053033</u>	487g..t.....	546
<u>AF053032</u>	487g..t.....	546
<u>AF053031</u>	487g..t.....	546
<u>AF053030</u>	487g..t.....	546
<u>AF053029</u>	487g..t.....	546
<u>AF053028</u>	487g..t.....	546
<u>AF053027</u>	487g..t.....	546
<u>AF053026</u>	487g..t.....	546
<u>AF053020</u>	487g..t.....	546
<u>AF053019</u>	487g..t.....	546
<u>AF053043</u>	487g..t.....	546
<u>X82301</u>	487g..t.....	546
<u>AF053052</u>	487c.....	546
<u>X82300</u>	490c.....	546
<u>A3004238</u>	487g.....c.....a.....c.....	546
<u>A3004237</u>	487g.....c.....a.....c.....	546
<u>X82296</u>	487g.....c.....a.....	546
<u>NC_001700</u>	15524g..g.....c.....a.....g.....	15583
<u>U20753</u>	15524g..g.....c.....a.....g.....	15583
<u>AF125145</u>	357t.....c.....c..t.a.c.....c.....	416
<u>AF125144</u>	357t.....g.....t.....c.....a.....c.....	415
<u>AF154975</u>	487g.....g.....c.....a.....g.....c.....	546
<u>A3051237</u>	487g.....g.....c.....a.....g.....c.....	546
<u>AF125149</u>	357g.....t.....g..c..t.a.....c.....	415
<u>empseq_0</u>	61	tccatcccttcatttatccatccagccccagcagcagccacccctatccctcacgag	120
<u>AY005809</u>	99	158
<u>AF053054</u>	547c.....	606
<u>AF053053</u>	547c.....	606
<u>AF053050</u>	547g.....c.....	606
<u>AF053049</u>	547g.....c.....	606
<u>AF053025</u>	547g.....g.....c.....	606
<u>AF053024</u>	547g.....g.....c.....	606
<u>AF053023</u>	547g.....g.....c.....	606
<u>AF053022</u>	547g.....g.....c.....	606
<u>AF053021</u>	547g.....g.....c.....	606
<u>AF053018</u>	547g.....c.....	606
<u>AF053051</u>	547g.....g.....c.....	606
<u>AF053048</u>	547g.....g.....c.....	606
<u>AF053047</u>	547g.....g.....c.....	606
<u>AF053046</u>	547g.....g.....c.....	606
<u>AF053045</u>	547g.....g.....c.....	606
<u>AF053044</u>	547g.....g.....c.....	606
<u>AF053042</u>	547g.....g.....c.....	606
<u>AF053041</u>	547g.....g.....c.....	606
<u>AF053040</u>	547g.....g.....c.....	606
<u>AF053039</u>	547g.....g.....c.....	606
<u>AF053038</u>	547g.....g.....c.....	606
<u>AF053037</u>	547g.....g.....c.....	606
<u>AF053036</u>	547g.....g.....c.....	606
<u>AF053035</u>	547g.....g.....c.....	606
<u>AF053034</u>	547g.....g.....c.....	606
<u>AF053033</u>	547g.....g.....c.....	606
<u>AF053032</u>	547g.....g.....c.....	606
<u>AF053031</u>	547g.....g.....c.....	606
<u>AF053030</u>	547g.....g.....c.....	606
<u>AF053029</u>	547g.....g.....c.....	606
<u>AF053028</u>	547g.....g.....c.....	606
<u>AF053027</u>	547g.....g.....c.....	606

<u>AY005E09</u>	219c.....	278
<u>AF05J054</u>	667c.....	726
<u>AF05J053</u>	667c.....	726
<u>AF05J050</u>	667t.a.....ct.....	726
<u>AF05J049</u>	667t.a.....ct.....	726
<u>AF05J025</u>	667t.a.....ct.....	726
<u>AF05J024</u>	667t.a.....ct.....	726
<u>AF05J023</u>	667t.a.....ct.....	726
<u>AF05J022</u>	667t.a.....ct.....	726
<u>AF05J021</u>	667t.a.....ct.....	726
<u>AF05J018</u>	667t.a.....ct.....	726
<u>AF05J051</u>	667t.a.....ct.....	726
<u>AF05J048</u>	667t.a.....ct.....	726
<u>AF05J047</u>	667t.a.....ct.....	726
<u>AF05J046</u>	667t.a.....ct.....	726
<u>AF05J045</u>	667t.a.....ct.....	726
<u>AF05J044</u>	667t.a.....ct.....	726
<u>AF05J042</u>	667t.a.....ct.....	726
<u>AF05J041</u>	667t.a.....ct.....	726
<u>AF05J040</u>	667t.a.....ct.....	726
<u>AF05J039</u>	667t.a.....ct.....	726
<u>AF05J038</u>	667t.a.....ct.....	726
<u>AF05J037</u>	667t.a.....ct.....	726
<u>AF05J036</u>	667t.a.....ct.....	726
<u>AF05J035</u>	667t.a.....ct.....	726
<u>AF05J034</u>	667t.a.....ct.....	726
<u>AF05J033</u>	667t.a.....ct.....	726
<u>AF05J032</u>	667t.a.....ct.....	726
<u>AF05J031</u>	667t.a.....ct.....	726
<u>AF05J030</u>	667t.a.....ct.....	726
<u>AF05J029</u>	667t.a.....ct.....	726
<u>AF05J028</u>	667t.a.....ct.....	726
<u>AF05J027</u>	667t.a.....ct.....	726
<u>AF05J026</u>	667t.a.....ct.....	726
<u>AF05J020</u>	667t.a.....ct.....	726
<u>AF05J019</u>	667t.a.....ct.....	726
<u>AF05J043</u>	667t.a.....ct.....	726
<u>X82301</u>	667t.a.....ct.....	726
<u>AF05J052</u>	667a.....	726
<u>X82300</u>	667a.....	726
<u>AB004238</u>	667c.....a.....t.....	726
<u>AB004237</u>	667c.....a.....t.....	726
<u>X82296</u>	667c.....a.....t.....	726
<u>NC_001700</u>	15704c.....a.....t.....	15763
<u>U20753</u>	15704c.....a.....t.....	15763
<u>AF125145</u>	537t.....nt.a.....c....t.c.....	596
<u>AF125144</u>	537t.....c.....gt..t.t.....	596
<u>AF154975</u>	667c.....c.....a.....gcc...c.c.....	726
<u>AB05J237</u>	667c.....c.....a.....gcc...t.c.....	726
<u>AF125149</u>	537t.....t.....t.a.....t.c.....	596
<u>cmpseq_0</u>	241	gccccatcccacccgacctgttaggagaccccgataactacatccccggccaaacccctca	300
<u>AY005B09</u>	279c.....	338
<u>AF05J054</u>	727a.....g.....	785
<u>AF05J053</u>	727a.....g.....	785
<u>AF05J050</u>	727	785
<u>AF05J049</u>	727a.....c.....	785
<u>AF05J025</u>	727a.....c.....	785
<u>AF05J034</u>	727a.....c.....	785
<u>AF05J023</u>	727a.....c.....	785
<u>AF05J022</u>	727a.....c.....	785
<u>AF05J021</u>	727a.....c.....	785
<u>AF05J018</u>	727a.....c.....	785
<u>AF05J051</u>	727a.....c.....	785
<u>AF05J049</u>	727a.....c.....	785
<u>AF05J047</u>	727a.....c.....	785
<u>AF05J046</u>	727a.....c.....	785
<u>AF05J045</u>	727a.....c.....	785
<u>AF05J044</u>	727a.....c.....	785
<u>AF05J043</u>	727a.....c.....	785
<u>AF05J042</u>	727a.....c.....	785
<u>AF05J041</u>	727a.....c.....	785

<u>AF053030</u>	727	a.....	c.....	c.....	c... 786
<u>AF053039</u>	727	a.....	c.....	c.....	c... 786
<u>AF053038</u>	727	a.....	c.....	c.....	c... 786
<u>AF053037</u>	727	a.....	c.....	c.....	c... 786
<u>AF053036</u>	727	a.....	c.....	c.....	c... 786
<u>AF053035</u>	727	a.....	c.....	c.....	c... 786
<u>AF053034</u>	727	a.....	c.....	c.....	c... 786
<u>AF053033</u>	727	a.....	c.....	c.....	c... 786
<u>AF053032</u>	727	a.....	c.....	c.....	c... 786
<u>AF053031</u>	727	a.....	c.....	c.....	c... 786
<u>AF053030</u>	727	a.....	c.....	c.....	c... 786
<u>AF053029</u>	727	a.....	c.....	c.....	c... 786
<u>AF053028</u>	727	a.....	c.....	c.....	c... 786
<u>AF053027</u>	727	a.....	c.....	c.....	c... 786
<u>AF053026</u>	727	a.....	c.....	c.....	c... 786
<u>AF053020</u>	727	a.....	c.....	c.....	c... 786
<u>AF053019</u>	727	a.....	t.....	c.....	c... 786
<u>AF053043</u>	727	a.....	t.....	c.....	c... 786
<u>X82301</u>	727	a.....	t.....	c.....	c... 786
<u>AF053052</u>	727	a.....t....c....t.c...c....t	c.....	c.....	c... 786
<u>X82300</u>	727	a.....t....c....c.....t.c...c....t	c.....	c.....	c... 786
<u>A3004238</u>	727	c.....	a..c.g.....a.....	c.....	c... 786
<u>A3004237</u>	727	c.....	a..c.....a.....	c.....	c... 786
<u>X82296</u>	727	r..t....c.....a.c.....a.....	c.....	c.....	c... 786
<u>NC_001700</u>	15764	t.....c.....a.c.....a.....	c.....	c.....	c... 15823
<u>U20753</u>	15764	t.....c.....a.c.....a.....	c.....	c.....	c... 15823
<u>AF125145</u>	597	t.....c.....a.c.....c.....a.....	c.....	c.....	c... 650
<u>AF125144</u>	597	t.....c.....a.c.....c.....a.....	c.....	c.....	c... 656
<u>AF154975</u>	727	a.....c.....c.g.....a.c.....c.....a..c	c.....	c.....	c... 786
<u>A3051237</u>	727	a.....c.....c.g.....a.c.....c.....a..c	c.....	c.....	c... 786
<u>AF125149</u>	597	t.....cc.....a.....c.c.....	c.....	c.....	c... 656
<u>empseq_0</u>	301	aataccccctccccatatacgccgtgaat	328		
<u>AY005809</u>	339	365		
<u>AF053054</u>	787	.c.....	808		
<u>AF053053</u>	787	.c.....	808		
<u>AF053050</u>	787t....c....	814		
<u>AF053049</u>	787t....c....	814		
<u>AF053025</u>	787c....c....	814		
<u>AF053024</u>	787t....c....	814		
<u>AF053023</u>	787c....c....	814		
<u>AF053022</u>	787c....c....	814		
<u>AF053021</u>	787t....c....	814		
<u>AF053018</u>	787t....c....	814		
<u>AF053051</u>	787t....c....	814		
<u>AF053048</u>	787t....c....	814		
<u>AF053047</u>	787t....c....	814		
<u>AF053046</u>	787t....c....	814		
<u>AF053045</u>	787t....c....	814		
<u>AF053044</u>	787t....c....	814		
<u>AF053042</u>	787c....c....	814		
<u>AF053041</u>	787t....c....	814		
<u>AF053040</u>	787c....c....	814		
<u>AF053039</u>	787t....c....	814		
<u>AF053038</u>	787t....c....	814		
<u>AF053037</u>	787t....c....	814		
<u>AF053036</u>	787t....c....	814		
<u>AF053035</u>	787t....c....	814		
<u>AF053034</u>	787t....c....	814		
<u>AF053033</u>	787c....c....	814		
<u>AF053032</u>	787c....c....	814		
<u>AF053031</u>	787c....c....	814		
<u>AF053030</u>	787c....c....	814		
<u>AF053029</u>	787c....c....	814		
<u>AF053028</u>	787c....c....	814		
<u>AF053027</u>	787c....c....	814		
<u>AF053026</u>	787c....c....	814		
<u>AF053020</u>	787c....c....	814		
<u>AF053012</u>	787c....c....	814		
<u>AF053001</u>	787c....c....	814		
<u>X82301</u>	787c....c....	814		

<u>AF053052</u>	787	.gc.....	a.....	812
<u>X82100</u>	787	.gc.....	a.....	814
<u>AB004238</u>	787	c..a.....	814
<u>AB004237</u>	787	c..a.....	814
<u>X82296</u>	787	c..a.....	814
<u>NC_001700</u>	15824	c..a.....	15851
<u>U20753</u>	15824	c..a.....	15851
<u>AF125144</u>	657	..c.....		664
<u>AF154975</u>	787	..c..a..a.....		803
<u>AB051237</u>	787	..c..a..a.....		803
<u>AF125149</u>	657	..c.....		664

Database: nt
 Posted date: Mar 2, 2001 12:20 AM
 Number of letters in database: 2,863,827,885
 Number of sequences in database: 807,597

Lambda K H
 1.37 0.711 1.31

Gapped Lambda K H
 1.37 0.711 1.31

Matrix: blastn matrix:1 -3
 Gap Penalties: Existence: 5, Extension: 2
 Number of Hits to DB: 460542
 Number of Sequences: 807597
 Number of extensions: 460542
 Number of successful extensions: 22671
 Number of sequences better than 10.0: 6487
 length of query: 328
 length of database: 2,863,827,885
 effective HSP length: 20
 effective length of query: 308
 effective length of database: 2,847,675,945
 effective search space: 877084191060
 effective search space used: 877084191060
 T: 0
 A: 30
 X1: 6 (11.9 bits)
 X2: 15 (29.7 bits)
 S1: 12 (24.3 bits)
 S2: 19 (38.2 bits)

Table 5. Reference animals and the allocated code numbers included in the study

SN.	Code number	Name of the animal	Zoological name
1	bhz25t	Indian tiger	<i>Panthera tigris tigris</i>
2	bhz26t	Indian tiger	<i>Panthera tigris tigris</i>
3	bhz30t	Indian tiger	<i>Panthera tigris tigris</i>
4	bhz45t	Indian tiger	<i>Panthera tigris tigris</i>
5	bhz56t	Indian tiger	<i>Panthera tigris tigris</i>
6	bhz63t	Indian tiger	<i>Panthera tigris tigris</i>
7	bhz20wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
8	bhz22wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
9	bhz23wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
10	bhz28wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
11	gz1l	Normal leopard	<i>Panthera pardus</i>
12	gz2l	Normal leopard	<i>Panthera pardus</i>
13	gz3l	Normal leopard	<i>Panthera pardus</i>
14	gz21cl	Clouded leopard	<i>Neofelis nebulosa</i>
15	gz22cl	Clouded leopard	<i>Neofelis nebulosa</i>
16	darz14sl	Snow leopard	<i>Panthera uncia</i>
17	darz15sl	Snow leopard	<i>Panthera uncia</i>
18	darz16sl	Snow leopard	<i>Panthera uncia</i>
19	sbz22al	Asiatic lion	<i>Panthera leo persica</i>
20	sbz38al	Asiatic lion	<i>Panthera leo persica</i>
21	sbz39al	Asiatic lion	<i>Panthera leo persica</i>
22	humsk	Human	<i>Homo sapiens sapiens</i>
23	chimss	Chimpanzee	<i>Pan sp.</i>

Table 6. Multiple sequence alignments of the cytochrome b sequences of reference animals with the sequence obtained from confiscated animal remain

sbz22al	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
sbz38al	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
sbz39al	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
adil.flesh	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCTACCCGTGACACGGATTCTTGCCCTTCAC	60
gz1nl	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCTACCCGTGACACGGATTCTTGCCCTTCAC	60
gz2nl	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCTACCCGTGACACGGATTCTTGCCCTTCAC	60
gz3nl	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
bhz23wt	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
bhz28wt	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
bhz22wt	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
bhz20wt	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
bhz63c	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
bhz26c	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
bhz30c	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
bhz45c	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
bhz25c	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
dz14sl	TGAATCTGAGGAGCCTTCTCACTACACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
dz15sl	TGAATCTGAGGAGCCTTCTCACTACACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
dz16sl	TGAATCTGAGGAGCCTTCTCACTACACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
gz21cl	TGAATCTGAGGAGCCTTCTCACTAGACAAAGCCACCCGTGACACGGATTCTTGCCCTTCAC	60
gz22cl	TGAATCTGAGGAGCCTACTCACTAGACAGCCCTAACCGATTCTCACCGATTCTCACCTTCAC	60
chimss	TGAATCTGAGGAGCCTACTCACTAGACAGTCCCACCCCTCACACGATTCTTACCCCTTCAC	60
humsk	TGAATCTGAGGAGCCTACTCACTAGACAGTCCCACCCCTCACACGATTCTTACCCCTTCAC	60

sbz22al	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCTCCATGAA	120
sbz38al	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCTCCATGAA	120
sbz39al	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCTCCATGAA	120
adil.flesh	TTCATCCTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG	120
gz1nl	TTCATCCTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG	120
gz2nl	TTCATCCTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG	120
gz3nl	TTCATCCTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG	120
bhz23wt	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
bhz28wt	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
bhz22wt	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
bhz20wt	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
bhz63c	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
bhz56c	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
bhz26c	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
bhz30c	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
bhz45c	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
bhz25c	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
dz14sl	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
dz15sl	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
dz16sl	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
gz21cl	TTCATCCTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120
gz22cl	TTTATCTTACCCCTTCAATTACACAGCCCTAACACATTCTACCTTACACGAA	120
chimss	TTCATCTGCCCTTCAATTACACAGCCCTAACACATTCTACCTTACACGAA	120
humsk	TTCATCTGCCCTTCAATTACACAGCCCTAACACATTCTACCTTACACGAA	120

sbz22al	ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCACATAAAA TTCCATTCCATGAA	130
sbz38al	ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCACATAAAA TTCCATTCCATGAA	130

sbz39al	ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAAATTCCATTCCATCCA	180
adil.flesh	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
gz1nl	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
gz2nl	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
gz3nl	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
bhz23wt	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
bhz28wt	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
bhz22wt	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
bhz20wt	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
bhz63t	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
bhz56t	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
bhz26t	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
bhz30t	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
bhz45t	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
bhz25t	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
dz14s1	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
dz15s1	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
dz16s1	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
gz21cl	ACAGGATCCAATAACCCCTCAGGAATGGTATCCGATTAGACAAAATTCCATTCCACCCA	180
gz22cl	ACAGGATCCAATAACCCCTCAGGAATGGTATCCGATTAGACAAAATTCCATTCCACCCA	180
chimss	ACAGGATCAAATAACCCCTGGAATCACCTCCCCTCGACAAAATTACCTTCCACCC	180
humsk	ACGGGATCAAACAACCCCTCAGGAATCACCTCCCATTCCGATAAAATCATCTTCCACCC	180

sbz22al	TACTATACAAATCAAAGATACTTAGGCCTTCTAGTACTAATCTTAACACTCATRACTACTC	240
sbz38al	TACTATACAAATCAAAGATACTTAGGCCTTCTAGTACTAATCTTAACACTCATRACTACTC	240
sbz39al	TACTATACAAATCAAAGATACTTAGGCCTTCTAGTACTAATCTTAACACTCATRACTACTC	240
adil.flesh	TACTACACAAATCAAAGATACTCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
gz1nl	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
gz2nl	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
gz3nl	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
bhz23wt	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
bhz28wt	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
bhz22wt	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
bhz20wt	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
bhz63t	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
bhz56t	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
bhz26t	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
bhz30t	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
bhz45t	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
bhz25t	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
dz14s1	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
dz15s1	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
dz16s1	TACTACACAAATCAAAGACATCTGGGCCTTCTAGTACTAATCTTAGCACTCATRACTACTC	240
gz21cl	TACTATACAAATCAAAGATACTTAGGCCTCTAGTTCTAATTCTAGGCCTCACACTACTT	240
gz22cl	TACTATACAAATCAAAGATACTTAGGCCTCTAGTTCTAATTCTAGGCCTCACACTACTT	240
chimss	TACTACACAAATCAAAGATACTCTGGCTTATTCTCTGCTTCTGCTTAATGACATTA	240
humsk	TACTACACAAATCAAAGACGCCCTCGGCTTACTCTGCTTCTGCTTAATGACATTA	240

sbz22al	GTCCTATTCTCACCGACCTATTAGGAGATCCCCGACAACCTATAACCCCCGGCAATCTCTA	300
sbz38al	GTCCTATTCTCACCGACCTATTAGGAGATCCCCGACAACCTATAACCCCCGGCAATCTCTA	300
sbz39al	GTCCTATTCTCACCGACCTATTAGGAGATCCCCGACAACCTATAACCCCCGGCAATCTCTA	300
adil.flesh	GTCCTATTCTCACCGACCTATTAGGAGATCCCCGACAACCTATAACCCCCGGCAATCTCTA	300
gz1nl	GTCCTATTCTCACCGACCTATTAGGAGACCCCCGATAACTACATCTGGCAACCCCTCTA	300
gz2nl	GTCCTATTCTCACCGACCTATTAGGAGACCCCCGATAACTACATCTGGCAACCCCTCTA	300
gz3nl	GTCCTATTCTCACCGACCTATTAGGAGACCCCCGATAACTACATCTGGCAACCCCTCTA	300
bhz23wt	GTCCTATTCTCACCGACCTATTAGGAGACCCCCGATAACTACATCTGGCAACCCCTCTA	300

bhz28wt	GTCCTATTCTCACCAGACCTATTAGGGGACCCCATAACTACATCCCCGCCAACCCCTCTA	300
bhz22wt	GTCCTATTCTCACCAGACCTATTAGGGGACCCCATAACTACATCCCCGCCAACCCCTCTA	300
bhz20wt	GTCCTATTCTCACCAGACCTATTAGGGGACCCCATAACTACATCCCCGCCAACCCCTCTA	300
bhz63c	GTCCTATTCTCACCAGACCTATTAGGGGACCCCATAACTACATCCCCGCCAACCCCTCTA	300
bhz56c	GTCCTATTCTCACCAGACCTATTAGGGGACCCCATAACTACATCCCCGCCAACCCCTCTA	300
bhz26c	GTCCTATTCTCACCAGACCTATTAGGGGACCCCATAACTACATCCCCGCCAACCCCTCTA	300
bhz30c	GTCCTATTCTCACCAGACCTATTAGGGGACCCCATAACTACATCCCCGCCAACCCCTCTA	300
bhz45c	GTCCTATTCTCACCAGACCTATTAGGGGACCCCATAACTACATCCCCGCCAACCCCTCTA	300
bhz25c	GTCCTATTCTCACCAGACCTATTAGGGGACCCCATAACTACATCCCCGCCAACCCCTCTA	300
dz14sl	GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCCTCTA	300
dz15sl	GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCCTCTA	300
dz16sl	GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCCTCTA	300
gz21c1	GTTCTATTCTCCCCAGACCTACTAGGAGACCCGTACATTACACTCCCCGCCAACCCCTCTA	300
gz22c1	GTTCTATTCTCCCCAGACCTACTAGGAGACCCGTACATTACACTCCCCGCCAACCCCTCTA	300
chimss	ACACTATTCTCACCAGACCTCTGGCGATCCAGACAACTATACCTAGCTAACCCCTTA	300
humsk	ACACTATTCTCACCAGACCTCTAGGCAGCCAGACAACTATACCTAGCTAACCCCTTA	300
***** * * * * *		
sbz22al	AGCACCCCTCCCCATATCAAAACCTGAAT	328
sbz38al	AGCACCCCTCCCCATATCAAAACCTGAAT	328
sbz39al	AGCACCCCTCCCCATATCAAAACCTGAAT	328
adil.flesh	AATACCCCTCCCCATATCAAGCCTGAAT	328
gz1nl	AATACCCCTCCCCATATCAAGCCTGAAT	328
gz2nl	AATACCCCTCCCCATATCAAGCCTGAAT	328
gz3nl	AATACCCCTCCCCATATCAAGCCTGAAT	328
bhz23wt	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz28wt	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz22wt	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz20wt	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz63c	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz56c	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz26c	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz30c	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz45c	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz25c	AACACCCCTCCCCATATCAAGCGCGAAT	328
dz14sl	AACACCCCTCCCCATATCAAGCGCGAAT	328
dz15sl	AACACCCCTCCCCATATCAAGCGCGAAT	328
dz16sl	AACACCCCTCCCCATATCAAGCGCGAAT	328
gz21c1	AATACCCCTCCCCATATCAAGCCTGAAT	328
gz22c1	AATACCCCTCCCCATATCAAGCCTGAAT	328
chimss	AACACCCCTCCCCACATTAACCGGAAT	328
humsk	AACACCCCTCCCCACATCAAGCGCGAAT	328
***** * * * * *		

Table 7a

Table 7b

Position	114	117	120	123	129	132	139	140	141	147	148	149	150	153	154	156	159	162	168	169	170	171	177	180	186	198	199	200	204	208	210
adult flesh	T	C	G	A	T	C	T	C	A	A	G	T	A	C	G	C	A	C	T	C	C	A	C	A	T	G	C	T			
gz1l	
gz2l	
bhz25t	C	T	T	
bhz26t	C	T	T	
bhz30t	C	T	T	
bhz45t	C	T	T	
bhz25tl	C	T	T	
bhz20wl	C	T	T	
bhz22wl	C	T	T	
bhz23wl	C	T	T	
dz14st	R	C	I	S	M	D	P	N	R	L	R	N	R	S	T	R	N	R	S	T	R	N	S	T	R	N	S	T			
dz15st	R	C	I	S	M	D	P	N	R	L	R	N	R	S	T	R	N	R	S	T	R	N	S	T	R	N	S	T			
gz22al	C	T	A	.	T	.	.	.	G	.	T	.	T	.	T	.	T	.	T	.	T	.	A		
gz23al	C	T	A	.	T	.	.	.	G	.	T	.	T	.	T	.	T	.	T	.	T	.	A		
gz21cl	C	T	A	.	C	T	.	.	G	.	T	.	C	.	G	.	T	.	T	.	T	.	A		
gz22cl	C	T	A	.	C	T	.	.	G	.	T	.	C	.	G	.	T	.	T	.	T	.	A		
dz10ts	R	A	S	A	R	A	M	S	T	M	G	N	K	A	C	N	T	A	N	M	K	A	T	N	M	K	A	T			
dz10tk	R	A	S	A	R	A	M	S	T	M	G	N	K	A	C	N	T	A	N	M	K	A	T	N	M	K	A	T			

Table 7c

Table 7d

Position	273	276	279	282	284	285	287	288	291	294	297	298	302	303	309	315	318	321	323	324
adll.flesh	C	T	C	C	T	C	C	T	C	C	T	C	A	T	T	T	T	C	G	C
gz11
bhz24t
bhz24wt
bhz25t	C	C	.	.	.	G	C	
bhz26t	C	C	.	.	.	G	C	
bhz30t	C	C	.	.	.	G	C	
bhz45t	C	C	.	.	.	G	C	
bhz56t	C	C	.	.	.	G	C	
bhz20wt	C	C	.	.	.	G	C	
bhz22wt	C	C	.	.	.	G	C	
bhz23wt	C	C	.	.	.	G	C	
dz14sl	C	C	.	.	.	C	C	
dz15sl	C	C	.	.	.	C	C	
sbz22al	.	C	.	T	C	.	.	C	.	T	.	.	G	C	.	.	A	.	.	
sbz38al	.	C	.	T	C	.	.	C	.	T	.	.	G	C	.	.	A	.	.	
gz21cl	T	C	T	.	C	T	.	C	.	T	.	.	G	C	
gz22cl	T	C	T	.	C	T	.	C	.	T	.	.	G	C	
chimss	T	A	T	C	T	A	T	C	T	A	T	C	T	A	T	C	T	C	C	
humsk	T	A	T	C	T	A	T	C	T	A	T	C	T	A	T	C	T	C	C	

Table 8. Percent similarity matrix calculated by pair-wise comparisons of cytochrome b gene sequences revealed from 'adl.flesh' and different feids

bhz20wt	bhz25t	dz14sl	humsk	chimss	sbz22al	gz1L	gz2L	gz3L	gz21cl	adl.flesh
[REDACTED]	100	99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
bhz25t	100	[REDACTED]	99.1	81.7	78.7	93.3	95.1	95.4	89.6	95.4
dz14sl	99.1	99.1	[REDACTED]	81.4	78.4	93	94.8	95.1	89.3	95.1
humsk	81.7	81.7	81.4	[REDACTED]	86.9	79.6	81.1	80.2	80.2	79
chimss	78.7	78.7	78.4	86.9	[REDACTED]	78.7	79.6	78.7	78.7	79.9
sbz22al	93.3	93	79.6	78.7	[REDACTED]	92.1	92.4	92.4	89	92.4
gz1L	95.1	95.1	94.8	81.1	79.6	92.1	[REDACTED]	98.5	98.5	99.3
gz2L	95.4	95.4	95.1	80.2	78.7	92.4	98.5	[REDACTED]	100	88.1
gz3L	95.4	95.4	95.1	80.2	78.7	92.4	98.5	100	[REDACTED]	88.1
gz21cl	89.6	89.6	89.3	79	76.8	89	89.3	88.1	[REDACTED]	89.6
adl.flesh	95.4	95.4	95.1	81.4	79.9	92.4	99.7	98.2	98.2	89.6

Table 1C



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 984591695-10075-13605

Query=

(25 letters)

Database:nt
807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQs

Taxonomy reportsDistribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

			Score (bits)	E Value
gb AF231651.1 AF231651	Strongylura notata clone HB-82 cytoc...	50	2e-05	
gb AF231650.1 AF231650	Strongylura notata clone HB-159 cyto...	50	2e-05	
ref NC_002672.1	Dinornis giganteus mitochondrion, complete...	50	2e-05	
ref NC_002673.1	Emeus crassus mitochondrion, complete genome	50	2e-05	
gb AF232015.1 AF232015	Nothrotheriops shastensis cytochrome...	50	2e-05	
gb AF232013.1 AF232013	Bradypus variegatus cytochrome b gen...	50	2e-05	
gb AY016019.1	Emeus crassus mitochondrion, complete genome	50	2e-05	
gb AY016013.1	Dinornis giganteus mitochondrion, complete g...	50	2e-05	
gb AY016014.1	Dromaius novaehollandiae mitochondrion, part...	50	2e-05	
gb AF230167.1 AF230167	Bonasa umbellus cytochrome b (CYTB) ...	50	2e-05	
gb AF074594.1 AF074594	Baeolophus bicolor cytochrome b gene...	50	2e-05	
gb AY005210.1	Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05	
gb AY005209.1	Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05	
gb AY005208.1	Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05	
gb AY005205.1	Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05	
gb AY005204.1	Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05	
gb AY005203.1	Poospiza erythrophrys cytochrome b (cytb) ge...	50	2e-05	
gb AY005201.1	Poospiza boliviana cytochrome b (cytb) gene, ...	50	2e-05	
gb AY005199.1	Poospiza alticola isolate 2 cytochrome b (cy...	50	2e-05	
gb AY005198.1	Poospiza alticola isolate 1 cytochrome b (cy...	50	2e-05	
gb AF155870.1 AF155870	Heterocephalus glaber cytochrome b (...)	50	2e-05	
gb AF189123.1 AF189123	Glyptotermes eukalypti cytochrome b ...	50	2e-05	
gb AF102099.1 AF102099	Criniferoides leucogaster cytochrome...	50	2e-05	
gb AF102095.1 AF102095S1	Corythaixoides concolor cytochrome...	50	2e-05	
gb AF271065.1 AF271065	Mustela erminea specimen-voucher AF1...	50	2e-05	
gb AF243857.1 AF243857	Strongylura notata notata cytochrome...	50	2e-05	
gb AF243856.1 AF243856	Strongylura notata forsythia cytochr...	50	2e-05	
ref NC_001567.1	Bos taurus mitochondrion, complete genome	50	2e-05	
gb AF306872.1 AF306872	Brachyramphus marmoratus haplotype M...	50	2e-05	
gb AF306871.1 AF306871	Brachyramphus marmoratus haplotype M...	50	2e-05	
gb AF306870.1 AF306870	Brachyramphus brevirostris haplotype...	50	2e-05	
gb AF306869.1 AF306869	Brachyramphus brevirostris haplotype...	50	2e-05	
gb AF306868.1 AF306868	Brachyramphus brevirostris haplotype...	50	2e-05	
gb AF010406.1 AF010406	Ovis aries complete mitochondrial ge...	50	2e-05	
gb AF248662.1 AF248662	Gryllus campestris haplotype 2 cytoc...	50	2e-05	
gb AF248661.1 AF248661	Gryllus campestris haplotype 1 cytoc...	50	2e-05	
gb AF096462.1 AF096462	Rhipidura albicollis cytochrome b ge...	50	2e-05	
gb AF283644.1 AF283644	Elaphe obsoleta cytochrome b gene, c...	50	2e-05	
gb AF283643.1 AF283643	Elaphe obsoleta cytochrome b gene, c...	50	2e-05	
gb AF283642.1 AF283642	Elaphe obsoleta cytochrome b gene, c...	50	2e-05	
gb AF283641.1 AF283641	Elaphe obsoleta cytochrome b gene, c...	50	2e-05	
gb AF283640.1 AF283640	Elaphe obsoleta cytochrome b gene, c...	50	2e-05	
gb AF283639.1 AF283639	Elaphe obsoleta cytochrome b gene, c...	50	2e-05	
gb AF283637.1 AF283637	Elaphe obsoleta LSUMZ 45359 cytochro...	50	2e-05	
gb AF283636.1 AF283636	Elaphe obsoleta LSUMZ 44662 cytochro...	50	2e-05	
gb AF283635.1 AF283635	Elaphe obsoleta LSUMZ 40443 cytochro...	50	2e-05	
gb AF283634.1 AF283634	Elaphe obsoleta LSUMZ 44335 cytochro...	50	2e-05	
gb AF283633.1 AF283633	Elaphe obsoleta LSUMZ 42624 cytochro...	50	2e-05	
gb AF283632.1 AF283632	Elaphe obsoleta LSUMZ H1911 cytochro...	50	2e-05	
gb AF283631.1 AF283631	Elaphe obsoleta LSUMZ 41197 cytochro...	50	2e-05	
gb AF283630.1 AF283630	Elaphe obsoleta LSUMZ 41189 cytochro...	50	2e-05	
gb AF283629.1 AF283629	Elaphe obsoleta LSUMZ 41188 cytochro...	50	2e-05	
gb AF283628.1 AF283628	Elaphe obsoleta LSUMZ 41187 cytochro...	50	2e-05	
gb AF283627.1 AF283627	Elaphe obsoleta LSUMZ 41186 cytochro...	50	2e-05	
gb AF283626.1 AF283626	Elaphe obsoleta LSUMZ 40943 cytochro...	50	2e-05	
gb AF283625.1 AF283625	Elaphe obsoleta LSUMZ 37499 cytochro...	50	2e-05	
gb AF283624.1 AF283624	Elaphe obsoleta LSUMZ 44480 cytochro...	50	2e-05	
gb AF283623.1 AF283623	Elaphe obsoleta LSUMZ 44451 cytochro...	50	2e-05	
gb AF283622.1 AF283622	Elaphe obsoleta LSUMZ 40444 cytochro...	50	2e-05	
gb AF283621.1 AF283621	Elaphe obsoleta LSUMZ 39925 cytochro...	50	2e-05	
gb AF283620.1 AF283620	Elaphe obsoleta LSUMZ 39163 cytochro...	50	2e-05	
gb AF283619.1 AF283619	Elaphe obsoleta LSUMZ 39162 cytochrom...	50	2e-05	
gb AF283618.1 AF283618	Elaphe obsoleta LSUMZ H15896 cytochro...	50	2e-05	
gb AF283617.1 AF283617	Elaphe obsoleta LSUMZ H15897 cytochro...	50	2e-05	
gb AF283616.1 AF283616	Elaphe obsoleta LSUMZ 15891 cytochro...	50	2e-05	
gb AF283615.1 AF283615	Elaphe obsoleta LSUMZ H15890 cytochro...	50	2e-05	
gb AF283614.1 AF283614	Elaphe obsoleta LSUMZ H15889 cytochro...	50	2e-05	
gb AF283613.1 AF283613	Elaphe obsoleta LSUMZ H15888 cytochro...	50	2e-05	

Table 9. Animals selected for validation of minimum P'S score for efficient amplification of DNA templates in PCR

SL.	Name	P, S/AFF	P, S/AFR
1	Indian black buck (<i>Antilope cervicapra</i>)	97, 58	96, 54
2	Sheep (<i>Ovis</i>	87, 53	96, 54
3	Pig (<i>Sus scrofa</i>)	87, 52	87, 41
4	Fresh water dolphin (<i>Platanista gangetica</i>)	86, 49	82, 47

Sequences producing significant alignments:

		Score (bits)	E Value
gb AF231651.1 AF231651	Strongylura notata clone HB-82 cytoc...	50	2e-05
gb AF231650.1 AF231650	Strongylura notata clone HB-159 cyto...	50	2e-05
ref NC_002672.1	Dinornis giganteus mitochondrion, complete...	50	2e-05
ref NC_002673.1	Emeus crassus mitochondrion, complete genome	50	2e-05
gb AF232015.1 AF232015	Nothrotheriops shastensis cytochrome...	50	2e-05
gb AF232013.1 AF232013	Bradypus variegatus cytochrome b gen...	50	2e-05
gb AY016015.1	Emeus crassus mitochondrion, complete genome	50	2e-05
gb AY016013.1	Dinornis giganteus mitochondrion, complete genome	50	2e-05
gb AY016014.1	Dromaius novaehollandiae mitochondrion, part...	50	2e-05
gb AF230167.1 AF230167	Bonasa umbellus cytochrome b (CYTB) ...	50	2e-05
gb AF074594.1 AF074594	Baeolophus bicolor cytochrome b gene...	50	2e-05
gb AY005210.1	Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05
gb AY005209.1	Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05
gb AY005208.1	Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05
gb AY005205.1	Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05
gb AY005204.1	Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05
gb AY005203.1	Poospiza erythroryphrys cytochrome b (cytb) ge...	50	2e-05
gb AY005201.1	Poospiza boliviana cytochrome b (cytb) gene, ...	50	2e-05
gb AY005199.1	Poospiza alticola isolate 2 cytochrome b (cy...	50	2e-05
gb AY005198.1	Poospiza alticola isolate 1 cytochrome b (cy...	50	2e-05
gb AF155870.1 AF155870	Heterocephalus glaber cytochrome b (...)	50	2e-05
gb AF189123.1 AF189123	Glyptotermes eukalypti cytochrome b ...	50	2e-05
gb AF102099.1 AF102099	Criniferoides leucogaster cytochrome...	50	2e-05
gb AF102095.1 AF102095S1	Corythaixoides concolor cytochrome...	50	2e-05
gb AF271065.1 AF271065	Mustela erminea specimen-voucher AF1...	50	2e-05
gb AF243857.1 AF243857	Strongylura notata notata cytochrome...	50	2e-05
gb AF243856.1 AF243856	Strongylura notata forsythia cytochr...	50	2e-05
ref NC_001967.1	Bos taurus mitochondrion, complete genome	50	2e-05
gb AF306872.1 AF306872	Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306871.1 AF306871	Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306870.1 AF306870	Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306869.1 AF306869	Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306868.1 AF306868	Brachyramphus brevirostris haplotype...	50	2e-05
gb AF010406.1 AF010406	Ovis aries complete mitochondrial ge...	50	2e-05
gb AF248662.1 AF248662	Gryllus campestris haplotype 2 cytoc...	50	2e-05
gb AF248661.1 AF248661	Gryllus campestris haplotype 1 cytoc...	50	2e-05
gb AF096462.1 AF096462	Rhipidura albicollis cytochrome b ge...	50	2e-05
gb AF283644.1 AF283644	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283643.1 AF283643	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283642.1 AF283642	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283641.1 AF283641	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283640.1 AF283640	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283639.1 AF283639	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283637.1 AF283637	Elaphe obsoleta LSUMZ 45359 cytochro...	50	2e-05
gb AF283636.1 AF283636	Elaphe obsoleta LSUMZ 44662 cytochro...	50	2e-05
gb AF283635.1 AF283635	Elaphe obsoleta LSUMZ 40443 cytochro...	50	2e-05
gb AF283634.1 AF283634	Elaphe obsoleta LSUMZ 44335 cytochro...	50	2e-05
gb AF283633.1 AF283633	Elaphe obsoleta LSUMZ 42624 cytochro...	50	2e-05
gb AF283632.1 AF283632	Elaphe obsoleta LSUMZ K1911 cytochro...	50	2e-05
gb AF283631.1 AF283631	Elaphe obsoleta LSUMZ 41197 cytochro...	50	2e-05
gb AF283630.1 AF283630	Elaphe obsoleta LSUMZ 41189 cytochro...	50	2e-05
gb AF283629.1 AF283629	Elaphe obsoleta LSUMZ 41188 cytochro...	50	2e-05
gb AF283628.1 AF283628	Elaphe obsoleta LSUMZ 41187 cytochro...	50	2e-05
gb AF283627.1 AF283627	Elaphe obsoleta LSUMZ 41186 cytochro...	50	2e-05
gb AF283626.1 AF283626	Elaphe obsoleta LSUMZ 40943 cytochro...	50	2e-05
gb AF283625.1 AF283625	Elaphe obsoleta LSUMZ 37499 cytochro...	50	2e-05
gb AF283624.1 AF283624	Elaphe obsoleta LSUMZ 44480 cytochro...	50	2e-05
gb AF283623.1 AF283623	Elaphe obsoleta LSUMZ 44451 cytochro...	50	2e-05
gb AF283622.1 AF283622	Elaphe obsoleta LSUMZ 40444 cytochro...	50	2e-05
gb AF283621.1 AF283621	Elaphe obsoleta LSUMZ 39925 cytochro...	50	2e-05
gb AF283620.1 AF283620	Elaphe obsoleta LSUMZ 39163 cytochro...	50	2e-05
gb AF283619.1 AF283619	Elaphe obsoleta LSUMZ 39162 cytochro...	50	2e-05
gb AF283618.1 AF283618	Elaphe obsoleta LSUMZ K15896 cytochro...	50	2e-05
gb AF283617.1 AF283617	Elaphe obsoleta LSUMZ K15897 cytochro...	50	2e-05
gb AF283616.1 AF283616	Elaphe obsoleta LSUMZ 15891 cytochro...	50	2e-05
gb AF283615.1 AF283615	Elaphe obsoleta LSUMZ K15890 cytochro...	50	2e-05
gb AF283614.1 AF283614	Elaphe obsoleta LSUMZ K15889 cytochro...	50	2e-05
gb AF283613.1 AF283613	Elaphe obsoleta LSUMZ K15888 cytochro...	50	2e-05

gb AF283612..1 AF283612	Elaphe obsoleta LSUMZ H15884 cytochr...	50	2e-05
gb AF283611..1 AF283611	Elaphe obsoleta LSUMZ H15031 cytochr...	50	2e-05
gb AF283610..1 AF283610	Elaphe obsoleta LSUMZ H15030 cytochr...	50	2e-05
gb AF283609..1 AF283609	Elaphe obsoleta CAS 169468 cytochrom...	50	2e-05
gb AF283608..1 AF283608	Elaphe obsoleta LSUMZ H14782 cytochr...	50	2e-05
gb AF283607..1 AF283607	Elaphe obsoleta LSUMZ H14781 cytochr...	50	2e-05
gb AF283606..1 AF283606	Elaphe obsoleta LSUMZ H14724 cytochr...	50	2e-05
gb AF283605..1 AF283605	Elaphe obsoleta cytochrome b gene. c...	50	2e-05
gb AF283604..1 AF283604	Elaphe obsoleta cytochrome b gene. c...	50	2e-05
gb AF283603..1 AF283603	Elaphe obsoleta LSUMZ H3388 cytochro...	50	2e-05
gb AF283602..1 AF283602	Elaphe obsoleta LSUMZ H3385 cytochro...	50	2e-05
gb AF283601..1 AF283601	Elaphe obsoleta LSUMZ H3384 cytochro...	50	2e-05
gb AF283600..1 AF283600	Elaphe bairdi LSUMZ H3382 cytochrome...	50	2e-05
gb AF283599..1 AF283599	Elaphe bairdi LSUMZ H3381 cytochrome...	50	2e-05
gb AF283598..1 AF283598	Elaphe obsoleta LSUMZ H3379 cytochro...	50	2e-05
gb AF283597..1 AF283597	Elaphe obsoleta LSUMZ 39616 cytochro...	50	2e-05
cb AF283596..1 AF283596	Elaphe obsoleta LSUMZ H3376 cytochro...	50	2e-05
gb AF283595..1 AF283595	Elaphe obsoleta LSUMZ H3345 cytochro...	50	2e-05
gb AF283594..1 AF283594	Elaphe obsoleta LSUMZ H3309 cytochro...	50	2e-05
gb AF283593..1 AF283593	Elaphe obsoleta LSUMZ H3306 cytochro...	50	2e-05
gb AF283592..1 AF283592	Elaphe obsoleta LSUMZ H3276 cytochro...	50	2e-05
gb AF283591..1 AF283591	Elaphe obsoleta LSUMZ H3246 cytochro...	50	2e-05
gb AF283590..1 AF283590	Elaphe obsoleta LSUMZ H3212 cytochro...	50	2e-05
gb AF283589..1 AF283589	Elaphe obsoleta LSUMZ H3209 cytochro...	50	2e-05
gb AF283588..1 AF283588	Elaphe obsoleta LSUMZ H3206 cytochro...	50	2e-05
cb AF283587..1 AF283587	Elaphe obsoleta LSUMZ H3191 cytochro...	50	2e-05
gb AF283586..1 AF283586	Elaphe obsoleta LSUMZ H3190 cytochro...	50	2e-05
gb AF283585..1 AF283585	Elaphe obsoleta LSUMZ H3189 cytochro...	50	2e-05
gb AF283584..1 AF283584	Elaphe obsoleta LSUMZ H3188 cytochro...	50	2e-05
cb AF283583..1 AF283583	Elaphe obsoleta LSUMZ H3186 cytochro...	50	2e-05
gb AF283582..1 AF283582	Elaphe obsoleta LSUMZ H3169 cytochro...	50	2e-05
cb AF283581..1 AF283581	Elaphe obsoleta CAS 203083 cytochrom...	50	2e-05
cb AF283580..1 AF283580	Elaphe obsoleta CAS 203079 cytochrom...	50	2e-05
gb AF283579..1 AF283579	Elaphe obsoleta LSUMZ H2286 cytochro...	50	2e-05
gb AF283578..1 AF283578	Elaphe obsoleta LSUMZ H208631 cytochrom...	50	2e-05
cb AF283577..1 AF283577	Elaphe obsoleta LSUMZ H2229 cytochro...	50	2e-05
gb AF283576..1 AF283576	Rhinophylla pumilio isolate TK46001 ...	50	2e-05
gb AF187030..1 AF187030	Poospiza hispaniolensis cytochrome b...	50	2e-05
cb AF310052..1 AF310052	Volatinia jacarina cytochrome b gene...	50	2e-05
gb AF310046..1 AF310046	Deinagkistrodon acutus cytochrome b ...	50	2e-05
gb AF171919..1 AF171919	Trimeresurus mucrosquamatus cytb gen...	50	2e-05
gb AF171897..1 AF171897	Agelaius cyanopus cytochrome b (cytb...	50	2e-05
gb AF290174..1 AF290174	Agelaius phoeniceus cytochrome b (cy...	50	2e-05
cb AF290173..1 AF290173	Quiscalus major cytochrome b (cytb) ...	50	2e-05
gb AF290171..1 AF290171	Amblycercus holosericeus cytochrome ...	50	2e-05
gb AF290170..1 AF290170	Volatinia jacarina cytochrome b (cyt...)	50	2e-05
gb AF290150..1 AF290150	Reichrodontomys zacatecae cytochrome...	50	2e-05
gb AF176252..1 AF176252	Reichrodontomys zacatecae cytochrome...	50	2e-05
gb AF176251..1 AF176251	Microtus xanthognathus cytochrome b ...	50	2e-05
gb AF163907..1 AF163907	Microtus pinetorum cytochrome b gene...	50	2e-05
gb AF163904..1 AF163904	Microtus ochrogaster cytochrome b ge...	50	2e-05
gb AF163901..1 AF163901	Microtus mizurus cytochrome b gene. c...	50	2e-05
gb AF163899..1 AF163899	Microtus californicus cytochrome B (...	50	2e-05
gb AF163891..1 AF163891	Microtus abbreviatus cytochrome B (c...	50	2e-05
gb AF163890..1 AF163890	Dipsochelys dussumieri isolate Germa...	50	2e-05
gb AF288524..1 AF288524	Dipsochelys dussumieri isolate white...	50	2e-05
gb AF288523..1 AF288523	Dipsochelys dussumieri isolate Aldy ...	50	2e-05
gb AF288522..1 AF288522	Psilopogon pyrolophus cytochrome b (...	50	2e-05
gb AF121530..1 AF121530	Eubucco bourcierii cucinkae cytochro...	50	2e-05
gb AF121512..1 AF121512	Adolfus vauereselli cytochrome b gen...	50	2e-05
gb AF206548..1 AF206548	Gymnorhina tibicen cytochrome b gene...	50	2e-05
gb AF197867..1 AF197867	Sitta europaea cytochrome b gene, part...	50	2e-05
gb U61197..2 SEU61197	Dinodon semicarinatus mitochondrion, compl...	50	2e-05
ref INC 001945..1	Oasypus novemcinctus mitochondrion, comple...	50	2e-05
ref INC 001861..1	Daeomyia incomta country Tanzania cy...	50	2e-05
gb AF141217..1 AF141217	Pantodon buchholzi cytochrome b gene...	50	2e-05
gb AF201615..1 AF201615	Bombus nevadensis cytochrome b gene....	50	2e-05
gb AF077930..1 AF077930	Oreamnos americanus cytochrome b (cy...	50	2e-05
gb AF199612..1 AF199612	taurus mitochondrion, complete genome	50	2e-05
gb J01192..1 B0VMT_808	Cochlearius cochlearius cytochrome b...	50	2e-05
gb AF191810..1 AF191810		50	2e-05

gb U85161.1 CAU85161	Chlorostilbon aureoventris cytochrome ...	50	2e-05
gb U84171.1 AFU84171	Asio flammeus cytochrome b (cytb) gene...	50	2e-05
gb AF217633.1 AF217633	Homoroselaps lacteus cytochrome b ge...	50	2e-05
gb AF217822.1 AF217822	Hydrophis semperi cytochrome b gene, ...	50	2e-05
gb AF217813.1 AF217813	Acanthophis antarcticus cytochrome b...	50	2e-05
gb AF220406.1 AF220408	Calliophis kelloggi cytochrome b (cy...)	50	2e-05
gb AF126430.1 AF126430	Ellobius fuscocapillus cytochrome b ...	50	2e-05
gb AF090337.1 AF090337	Aythya americana mitochondrion, comp...	50	2e-05
gb AF059111.1 AF059111	Sarkidiornis melanotos cytochrome b ...	50	2e-05
gb AF099053.1 AF099053	Aix sponsa cytochrome b gene, partia...	50	2e-05
gb AF099308.1 AF099308	Icterus wagleri wagleri cytochrome b...	50	2e-05
gb AF099295.1 AF099295	Icterus gularis yucatanensis cytochr...	50	2e-05
gb AF099294.1 AF099294	Icterus gularis tamaulipensis cytoch...	50	2e-05
gb AF099293.1 AF099293	Icterus gularis gularis cytochrome b...	50	2e-05
gb AF160610.1 AF160610	Cricetomys emini Cemi636 cytochrome ...	50	2e-05
gb AF036280.1 AF036280	Tragelaphus strepsiceros cytochrome ...	50	2e-05
gb AF036277.1 AF036277	Tragelaphus scriptus cytochrome b (c...	50	2e-05
gb AF036274.1	Tetracerus quadricornis cytochrome b (cytb) ...	50	2e-05
gb AF194218.1 AF194218	Phrynosoma platyrhinos cytochrome b ...	50	2e-05
gb AF194216.1 AF194216	Urosaurus ornatus cytochrome b gene, ...	50	2e-05
ref NC_002009.1	Artibeus jamaicensis mitochondrion, comple...	50	2e-05
ref NC_001941.1	Ovis aries mitochondrion, complete genome	50	2e-05
ref NC_000877.1	Aythya americana mitochondrion, complete g...	50	2e-05
ref NC_000846.1	Rhea americana mitochondrion, complete genome	50	2e-05
gb U27551.1 GCU27551	Grus canadensis tabida cytochrome b (c...	50	2e-05
gb AF089058.1 AF089058	Quiscalus quiscula cytochrome b (cyt...)	50	2e-05
gb AF089055.1 AF089055	Quiscalus major cytochrome b (cytb) ...	50	2e-05
gb AF089054.1 AF089054	Quiscalus lugubris cytochrome b (cyt...)	50	2e-05
gb AF089046.1 AF089046	Oreopsar bolivianus cytochrome b (cy...)	50	2e-05
gb AF089042.1 AF089042	Molothrus badius cytochrome b (cytb) ...	50	2e-05
gb AF089039.1 AF089039	Macroagelaius imthurni cytochrome b ...	50	2e-05
gb AF089037.1 AF089037	Lampropsartanagrinus cytochrome b (...)	50	2e-05
gb AF089026.1 AF089026	Gymnomystax mexicanus cytochrome b (...)	50	2e-05
gb AF089025.1 AF089025	Gnorimopsar chopi cytochrome b (cytb...)	50	2e-05
gb AF089024.1 AF089024	Euphagus cyanocephalus cytochrome b ...	50	2e-05
gb AF089023.1 AF089023	Euphagus carolinus cytochrome b (cyt...)	50	2e-05
gb AF089021.1 AF089021	Dives warzewitschi cytochrome b (cyt...)	50	2e-05
gb AF089020.1 AF089020	Curaeus curaeus cytochrome b (cytb) ...	50	2e-05
gb AF089016.1 AF089016	Amblycercus holosericeus cytochrome ...	50	2e-05
gb AF089013.1 AF089013	Agelaius xanthophthalmus cytochrome ...	50	2e-05
gb AF089012.1 AF089012	Agelaius xanthomus cytochrome b (cyt...)	50	2e-05
gb AF089008.1 AF089008	Agelaius phoeniceus sub-species phoe...	50	2e-05
gb AF089006.1 AF089006	. Agelaius humeralis cytochrome b (cyt...)	50	2e-05
gb AF089005.1 AF089005	Agelaius cyanopus cytochrome b (cytb...)	50	2e-05
gb AF108695.1 AF108696	Scolomys jamaicensis cytochrome B (cyt...)	50	2e-05
gb AF108685.1 AF108685	Wiedomys pyrrhorhinos cytochrome B (...)	50	2e-05
gb AF108677.1 AF108677	Thomasomys oreas cytochrome B (cytB) ...	50	2e-05
gb AF145511.1 AF145511	Melanoplus foedus cytochrome b gene, ...	50	2e-05
gb AF145511.1 AF145511	Melanoplus angustipennis cytochrome ...	50	2e-05
gb U89527.1 BMU89527	Bolitoglossa marmorea cytochrome b (cy...)	50	2e-05
gb U89523.1 BPU89523	Batrachoseps pacificus cytochrome b (c...	50	2e-05
gb AF181470.1 AF181470	Okapia johnstoni cytochrome b gene, ...	50	2e-05
gb AF084075.1 AF084075	Lagenostomus acutus cytochrome b g...	50	2e-05
gb U90303.1 OMU90303	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90302.1 OMU90302	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90301.1 OMU90301	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90300.1 OMU90300	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb AF038883.1 AF038883	Deinagkistrodon acutus cytochrome b ...	50	2e-05
gb AF039268.1 AF039268	Agkistrodon constrictor cytochrome b ...	50	2e-05
gb AF039267.1 AF039267	Boa constrictor cytochrome b (cytb) ...	50	2e-05
gb S49215.1 S49215	apocytochrome b (sheep, domestic, Merino...)	50	2e-05
gb AF158698.1 AF158698	Geomys pinetis cytochrome b gene, co...	50	2e-05
gb AF158692.1 AF158692	Geomys bursarius jugosuscularis cyto...	50	2e-05
gb AF058193.1 AF058193	Ithaginis cruentus cytochrome b (cyt...)	50	2e-05
gb AF091629.1 AF091629	Antilocapra americana cytochrome b (...)	50	2e-05
gb AF022061.1	Tragelaphus strepsiceros cytochrome b (cytb) ...	50	2e-05
gb AF022062.1	Tragelaphus derbianus cytochrome b (cytb) ge...	50	2e-05
gb AF022050.1	Hippotragus equinus cytochrome b (cytb) gene...	50	2e-05
gb AF022057.1	Tragelaphus oxyx cytochrome b (cytb) gene, m...	50	2e-05
gb AF111500.1 AF111500	Lagenostomus scutus isolate LACU74 ...	50	2e-05
gb AF111499.1 AF111499	Lagenostomus scutus isolate LACU77 ...	50	2e-05

gb UC4640.1 LB069695	Loxocemus bicolor cytochrome b (cytb) ...	50	2e-05
gb UE5910.1 EMU696010	Eunectes notaeus cytochrome b (cytb) S...	50	2e-05
gb UC5908.1 EMU696006	Eunectes murinus cytochrome b (cytb) S...	50	2e-05
gb U69799.1 ESU697994	Epicrates striatus fosteri cytochrome ...	50	2e-05
gb U69796.1 ESU69796	Epicrates striatus strigilatus cytochr...	50	2e-05
gb U69795.1 ESU69795	Epicrates striatus strigilatus cytochr...	50	2e-05
gb U69794.1 ESU69794	Epicrates striatus mcraniei cytochrom...	50	2e-05
gb U69793.1 ESU69793	Epicrates striatus mcraniei cytochrom...	50	2e-05
gb U69792.1 EMU69792	Epicrates monensis cytochrome b (cytb) ...	50	2e-05
gb U69790.1 EMU69790	Epicrates monensis cytochrome b (cytb) ...	50	2e-05
cb U69786.1 EFU69786	Epicrates fordii cytochrome b (cytb) ge...	50	2e-05
gb U69784.1 EFU69784	Epicrates fordii cytochrome b (cytb) ge...	50	2e-05
gb U69779.1 ECU69779	Epicrates cenchria cytochrome b (cytb) ...	50	2e-05
gb U69777.1 ECU69777	Epicrates cenchria cytochrome b (cytb) ...	50	2e-05
cb U69776.1 EAU69776	Epicrates angulifer cytochrome b (cytb...)	50	2e-05
gb U69774.1 EAU69774	Epicrates angulifer cytochrome b (cytb...)	50	2e-05
cb U69772.1 CEU69772	Corallus enydris cytochrome b (cytb) g...	50	2e-05
cb U69771.1 CEU69771	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69770.1 CEU69770	Corallus enydris cytochrome b (cytb) g...	50	2e-05
cb U69769.1 CEU69769	Corallus enydris cytochrome b (cytb) g...	50	2e-05
cb U69752.1 CAU69752	Candoia aspera cytochrome b (cytb) gen...	50	2e-05
gb U69746.1 BCU69746	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
cb U69740.1 BCU69740	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
cb AF139057.1 AF139057	Isoodon macrourus cytochrome b gene,...	50	2e-05
gb AF090339.1 AF090339	Rhea americana mitochondrion, comple...	50	2e-05
cb AF006275.1 AF006275	Cnemidophorus tigris strain Isla Ang...	50	2e-05
cb AF006267.1 AF006267	Cnemidophorus tigris strain Isla Smi...	50	2e-05
cb AF034969.1 AF034969	Connochaetes taurinus cytochrome b S...	50	2e-05
cb AF028822.1 AF028822	Alcelaphus buselaphus cytochrome b S...	50	2e-05
cb AF028821.1 AF028821	Damaliscus lunatus cytochrome b gene...	50	2e-05
gb AF061340.1 AF061340	Artibeus jamaicensis mitochondrial D...	50	2e-05
gb AF076093.1 AF076093	Thalassarche impavida cytochrome b (...)	50	2e-05
gb AF076091.1 AF076091	Thalassarche carteri cytochrome b (c...	50	2e-05
cb AF076072.1 AF076072	Pelagodroma marina cytochrome b (cyt...)	50	2e-05
cb AF076063.1 AF076063	Oceanodroma furcata cytochrome b (cy...	50	2e-05
cb AF076059.1 AF076059	Hydrobates pelagicus cytochrome b (c...	50	2e-05
cb AF076056.1 AF076056	Garradina nereis cytochrome b (cytb) ...	50	2e-05
cb AF076053.1 AF076053	Fregata tropica cytochrome b (cytb) ...	50	2e-05
cb AF076050.1 AF076050	Diomedea gibsoni cytochrome b (cytb) ...	50	2e-05
gb AF076049.1 AF076049	Diomedea epomophora cytochrome b (cy...	50	2e-05
gb AF076048.1 AF076048	Diomedea chionoptera cytochrome b (c...	50	2e-05
gb AF076047.1 AF076047	Diomedea antipodensis cytochrome b (...)	50	2e-05
gb U83314.1 MSU83314	Micrastur semitorquatus cytochrome b (...)	50	2e-05
cb U83318.1 MEU83318	Microhierax erythrogenys cytochrome b ...	50	2e-05
cb U37303.1 SAU37303	Synthliboramphus antiquus cytochrome b...	50	2e-05
gb U37302.1 PAU37302	Psychotramphus aleuticus cytochrome b S...	50	2e-05
cb U37296.1 CPU37296	Cyclorrhynchus psittacula cytochrome b...	50	2e-05
gb U37289.1 BHU37289	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U37286.1 APU37286	Aethia pygmaea cytochrome b gene, mito...	50	2e-05
gb U37104.1 APU37104	Aethia pusilla cytochrome b gene, mito...	50	2e-05
gb U37087.1 ACU37087	Aethia cristatella cytochrome b gene, ...	50	2e-05
gb U87525.1 HGU87525	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87524.1 HGU87524	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87523.1 HGU87523	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87522.1 HGU87522	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U17864.1 STU17864	Saiga tatarica cytochrome b gene, mito...	50	2e-05
gb U17863.1 OAU17863	Oreamnos americanus cytochrome b gene...	50	2e-05
gb U17862.1 OMU17862	Ovis moschatus moschatus cytochrome ...	50	2e-05
gb U17860.1 ODU17860	Ovis dalli cytochrome b gene, mitochon...	50	2e-05
gb U17859.1 OCU17859	Ovis canadensis cytochrome b gene, mit...	50	2e-05
gb U55274.1 TB065274	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65267.1 TB065267	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65260.1 TB065260	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65301.1 PAU65301	Perognathus amplus cytochrome b (cytb) ...	50	2e-05
gb AF034739.1 AF034739	Capra aegagrus cytochrome b (cytb) S...	50	2e-05
gb AF034738.1 Capra caucasica	caucasica cytochrome b (cytb) gene, mi...	50	2e-05
gb AF034737.1 Capra cylindricornis	cytochrome b (cytb) gen...	50	2e-05
gb AF034736.1 AF034736	Capra falconeri cytochrome b (cytb) ...	50	2e-05
gb AF034735.1 Capra ibex	cytochrome b (cytb) gene, mitochro...	50	2e-05
gb AF034730.1 AF034730	Ovis aries cytochrome b (cytb) gene...	50	2e-05
gb AF034729.1 AF034729	Ovis vignei cytochrome b (cytb) gene...	50	2e-05

gb AF034724.1	Ovis dalli dalli cytochrome b (cytb) gene, m...	50	2e-05
gb AF034727.1	Ovis ammon darwini cytochrome b (cytb) gene...	50	2e-05
gb AF034728.1 AF034724	Pantholops hodgsoni cytochrome b (cyt... Taxidea taxus cytochrome b (cytb) ge...	50	2e-05
gb U94805.1 TMU94805	Trogon melanurus cytochrome b gene, mito...	50	2e-05
gb U94804.1 TCU94804	Trogon comptus cytochrome b gene, mito...	50	2e-05
gb U94803.1 TVU94803	Trogon viridis cytochrome b gene, mito...	50	2e-05
gb AF006251.1 AF006251	Sericossypha albocristata cytochrome...	50	2e-05
gb AF006249.1 AF006249	Pyrrhocoma ruficeps cytochrome b (cyt... Lamprospiza melanoleuca cytochrome b...	50	2e-05
gb AF006234.1 AF006234	Hemispingus atropileus cytochrome b ... Cypsnagra hirundinacea cytochrome b ...	50	2e-05
gb AF006215.1 AF006215	Chlorophanes spiza cytochrome b (cyt... Chlorochrysa calliparaea cytochrome ...	50	2e-05
gb AF006214.1 AF006214	Calochaetes coccineus cytochrome b (... Buchraupis montana cytochrome b (cyt... Rupicapra rupicapra rupicapra mito...	50	2e-05
emb AJ293419.1 RRU293419	Rupicapra rupicapra rupicapra mito...	50	2e-05
emb AJ293416.1 RPPY293416	Rupicapra pyrenaica pyrenaica mito...	50	2e-05
emb AJ293415.1 RPPY293415	Rupicapra pyrenaica parva mitochon...	50	2e-05
emb AJ293414.1 RPPY293414	Rupicapra pyrenaica ornata mitoch...	50	2e-05
emb AJ293412.1 RRU293412	Rupicapra rupicapra rupicapra mito...	50	2e-05
emb AJ293418.1 CFA293418	Capra falconeri mitochondrial part...	50	2e-05
gb U07578.1 DCU07578	Dasyurus cristicauda mitochondrial c...	50	2e-05
emb AJ004180.1 HPAJ4180	Hydrobates pelagicus mitochondrial ...	50	2e-05
emb Y15695.1 SMY15695	Schilbe mystus mitochondrial cyt b gen...	50	2e-05
emb Y15697.1 EDY15697	Eutropius depressirostris mitochondrial...	50	2e-05
emb Y15696.1 EDY15696	Eutropius depressirostris mitochondrial...	50	2e-05
gb AF015035.1 AF015035	Steatocranus casuarius 20 cytochrom...	50	2e-05
gb AF015761.1 AF015761	Palmeria dolei cytochrome b (Cytb) g...	50	2e-05
gb AF015758.1 AF015758	Oreomystis mana cytochrome b (Cytb) ...	50	2e-05
gb AF015756.1 AF015756	Vestriaria coccinea cytochrome b (Cyt... Himatione sanguinea cytochrome b (Cyt... Dromaius novaehollandiae cytochrome b ...	50	2e-05
cb U76052.1 DNUT6052	Clethrionomys glareolus mitochondrial...	50	2e-05
emb AJ236634.1 CGL236634	Pelecanus onocrotalus cytochrome B gen...	50	2e-05
cb U83158.1 POU83158	Pelecanus onocrotalus cytochrome B gen...	50	2e-05
cb U83157.1 POU83157	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
cb U83156.1 AAU83156	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
cb U83155.1 AAU83155	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
cb U83154.1 AAU83154	Chelodina longicollis cytochrome b gen...	50	2e-05
cb U81356.1 CLU81356	Elaphe scalaris mitochondrial part...	50	2e-05
emb AJ277676.1 ESC277676	Elaphe scalaris mitochondrial part...	50	2e-05
emb AJ277675.1 ESC277675	Elaphe longissima mitochondrial pa...	50	2e-05
emb AJ277672.1 ELO277672	Elaphe longissima mitochondrial pa...	50	2e-05
emb AJ277671.1 ELO277671	Elaphe scalaris mitochondrial part...	50	2e-05
emb Y11832.1 MTCNCOMGN	Dasyurus novemcinctus compleze mitoch...	50	2e-05
emb AJ388467.1 NBA388467	Nemacheilus barbatulus mitochondrial...	50	2e-05
emb AJ388468.1 IME388468	Ictalurus melas mitochondrial cyt b...	50	2e-05
emb AJ388459.1 LDE388459	Leucaspis delineatus mitochondrial...	50	2e-05
gb U46167.1 SCU46167	Sciurus carolinensis cytochrome b gene...	50	2e-05
emb AJ245573.1 SIN245573	Schilbe intermedius partial mitoch...	50	2e-05
emb AJ245538.1 SIN245538	Schilbe intermedius partial mitoch...	50	2e-05
emb AJ245678.1 EDE245678	Eutropius depressirostris partial ...	50	2e-05
emb AJ245577.1 EDE245577	Eutropius depressirostris partial ...	50	2e-05
emb AJ245576.1 EDE245576	Eutropius depressirostris partial ...	50	2e-05
emb AJ245575.1 EDE245575	Eutropius depressirostris partial ...	50	2e-05
emb AJ245674.1 EDE245674	Eutropius depressirostris partial ...	50	2e-05
emb Y15884.3 MTRACOMPL	Rhea americana complete mitochondrial...	50	2e-05
gb U60768.1 PCU60768	Parus cinctus cytochrome b gene, mitoc...	50	2e-05
gb U482955.1 TMU482955	Thalassarche melanophris melanophris c...	50	2e-05
gb U489954.1 TCU489954	Thalassarche chrysostoma cytochrome b ...	50	2e-05
gb U489944.1 TCU489944	Thalassarche chlorostethos chlorosthy...	50	2e-05
gb U489943.1 PPU489943	Phoebebetria palpebrata cytochrome b (cyt... Phoebebetria fusca cytochrome b (cytb) g...	50	2e-05
gb U489942.1 PFU489942	Macronectes giganteus cytochrome b (cyt... Diomedea exulans dabbenena cytochrome ...	50	2e-05
gb U489947.1 DEV489947	Diomedes epomophora sanfordi cytochrom...	50	2e-05
gb U489946.1 DEV489946	Diomedes amsterdamensis cytochrome b (... Piranga rubra cytochrome b gene, mitoc...	50	2e-05
gb U489945.1 DAU489945	Actites hypoleucos cytochrome b (cyt... Actites hypoleucos cytochrome b (cytb) ...	50	2e-05
gb U555735.1 PRV15735	Actites hypoleucos cytochrome b (cytb) ...	50	2e-05
gb U555908.1 API555908	Actites hypoleucos cytochrome b (cyt... Actites hypoleucos cytochrome b (cytb) ...	50	2e-05
gb U555907.1 AQU555907	Actites hypoleucos cytochrome b (cyt... Actites hypoleucos cytochrome b (cytb) ...	50	2e-05
gb U555906.1 AQU555906	Actites hypoleucos cytochrome b (cyt... Actites hypoleucos cytochrome b (cytb) ...	50	2e-05

gb U66505_1 ALUCC505	Artibeus lituratus cytochrome b (cytb) ...	50	2e-05
gb U66504_1 AJU66504	Artibeus jamaicensis cytochrome b (cyt...)	50	2e-05
gb U66503_1 AJU66503	Artibeus jamaicensis cytochrome b (cyt...)	50	2e-05
gb U66502_1 AIU66502	Artibeus intermedius cytochrome b (cyt...)	50	2e-05
gb U66501_1 AJU66501	Artibeus inopinatus cytochrome b (cytb...)	50	2e-05
gb U66500_1 AHU66500	Artibeus hirsutus cytochrome b (cytb) ...	50	2e-05
gb U66499_1 AFU66499	Artibeus fraterculus cytochrome b (cyt...)	50	2e-05
gb U66498_1 AFU66498	Artibeus fimbriatus cytochrome b (cytb...)	50	2e-05
gb U63061_1 BBU63061	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U63060_1 BBU63060	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U63059_1 BBU63059	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U63058_1 BBU63058	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U58386_1 SJUS8386	Scolomys juruaense cytochrome b (cyt-b...)	50	2e-05
gb L11905_1 CGYMTCYTB0	Cratogeomys gymnurus mitochondrial c...	50	2e-05
gb U14672_1 MNU34672	Mecachirus nudicaudatus cytochrome b l...	50	2e-05
gb U14671_1 MNU34671	Mecachirus nudicaudatus cytochrome b l...	50	2e-05
emb Y14951_1 MTY14951	Capreolus capreolus mitochondrial cyt...	50	2e-05
emb Y14371_1 MTCCCYTB3	Capreolus capreolus mitochondrial cyt...	50	2e-05
gb L11909_1 CGYMTCYTB4	Cratogeomys tylorhinus mitochondrial...	50	2e-05
gb L11901_1 PPGNTCYTB8	Geomys bursarius juggosicularis mito...	50	2e-05
gb L11904_1 CGYMTCYTB3C	Cratogeomys goldmani goldmani mitoch...	50	2e-05
emb X94938_1 SPCYTB8	S.putorius mitochondrial DNA for cytoch...	50	2e-05
gb U46770_1 ARU46770	Anchus richardii cytochrome b gene, mit...	50	2e-05
gb U46769_1 ABU46769	Anchus berthelotii cytochrome b gene, ...	50	2e-05
gb U46183_1 SSU46183	Sciurus scammeneus cytochrome b gene, ...	50	2e-05
emb Y10728_1 PSMY10728	P.schwarzi mitochondrial cytb gene, ...	50	2e-05
emb X95768_1 NLMC8	N.leucopterus mitochondrial cytochrome b...	50	2e-05
emb X95767_1 NGRIMC9	N.griseus mitochondrial cytochrome b gene	50	2e-05
emb X86763_1 MTVGCYT26	V.Grypus mitochondrial cytB gene	50	2e-05
emb X86754_1 MTLCCYT17	L.crumeniferus mitochondrial cytb gene	50	2e-05
emb X96743_1 MTCACYT6	C.aura mitochondrial cytb gene	50	2e-05
dbj A3035242_1 A3035242	Pantodon buchholzi mitochondrial cy...	50	2e-05
emb X50946_1 MITDCB33	T.dorbignyi mitochondrial gene for c...	50	2e-05
emb AJ000029_1 MIRTCYB29	Rangifer tarandus mitochondrial cy...	50	2e-05
emb X82302_1 MIPFCYTB6	P.fasciata mitochondrial cytochrome ...	50	2e-05
emb X56291_1 MIIOHCYT8	O.hemicrus mitochondrion cytb gene fo...	50	2e-05
emb X56284_1 MOACYT8	O.aries mitochondrion cytb gene for c...	50	2e-05
emb AJ000022_1 MIMSCYB22	Dama dama mitochondrial cytb gene	50	2e-05
emb X72005_1 MILWCYT8	L.weddelli mitochondrial gene for cyt...	50	2e-05
emb Y09814_1 MIHLCYTB8	H.liberiensis mitochondrial cytochro...	50	2e-05
emb X60942_1 MIGTCB11	Gymnorhina tibicen mitochondrial gene...	50	2e-05
emb X56290_1 MIDDCYT8	D.dama mitochondrion cytb gene for cy...	50	2e-05
emb AJ000021_1 MICECYB21	Cervus elaphus mitochondrial cytb ...	50	2e-05
emb AJ000024_1 MICCCYB24	Capreolus capreolus mitochondrial ...	50	2e-05
emb V00654_1 MI3TXX	Bos taurus complete mitochondrial genome	50	2e-05
emb X36286_1 MIAACYT8A	A.americana mitochondrion cytb gene ...	50	2e-05
cb L19718_1 AIUMTCYTB8	Artibeus lituratus mitochondrial cyto...	50	2e-05
gb U27543_1 BRU27543	Balearica regulorum cytochrome b (cytb...)	50	2e-05
cbj A8030025_1 A8030025	Sciurus scammeneus mitochondrial cy...	50	2e-05
gb U18298_1 SCU18298	Spharagemon campestris cytochrome b ge...	50	2e-05
gb U18297_1 SCU18297	Spharagemon colilare cytochrome b gene...	50	2e-05
gb U18293_1 TPU18293	Trimerotropis picturaria cytochrome b...	50	2e-05
gb U18290_1 CPU18290	Cannula pellucida cytochrome b gene, m...	50	2e-05
gb U17904_1 CCU17904	Circotettix carlinianus mitochondrion ...	50	2e-05
cbj D84202_1 GOTMTCB8	Capsa falconeri mitochondrial DNA for ...	50	2e-05
cbj D84289_1 D84289	Bos javanicus mitochondrial DNA for cyt...	50	2e-05
cbj D32195_1 CCRMTCB25	Capricornis sumatrensis mitochondrial...	50	2e-05
cbj D32191_1 CCRMTCB21	Capricornis crispus mitochondrial ge...	50	2e-05
cbj AB021098_1 AB021098	Cervus elaphus kamsuensis mitochondr...	50	2e-05
cbj AB021097_1 AB021097	Cervus elaphus xanthopygus mitochondr...	50	2e-05
cbj AB021095_1 AB021095	Cervus nippon yesoensis mitochondri...	50	2e-05
cbj AB021094_1 AB021094	Cervus nippon centralis mitochondri...	50	2e-05
cbj AB021093_1 AB021092	Cervus nippon mageshimaensis mitochon...	50	2e-05
cbj AB021091_1 AB021091	Cervus nippon kuromarae mitochondrial...	50	2e-05
cbj AB001612_1 AB001612	Cervus elaphus mitochondrial DNA fo...	50	2e-05
cbj D84209_1 SHPMTCB8	Sheep mitochondrial DNA for cytochrom...	50	2e-05
cbj D84201_1 SHPMTCB8C	Ovis musimon mitochondrial DNA for cy...	50	2e-05
cbj D84206_1 BOVMTCB8	Bos javanicus mitochondrial gene for cy...	50	2e-05
cbj D84205_1 BOVMTCB8A	Bovine mitochondrial gene for cytochro...	50	2e-05
cbj D84208_1 ORMMTCB8	Oreamnos americanus mitochondrial ge...	50	2e-05
cbj D84205_1 MACMTCB8	Marmota flaviventris mitochondrial gene...	50	2e-05

dbj S32142.1 CEUMTCB11	Cervus nippon mitochondrial gene for...	50	2e-05
dbj AB021044.1 AB021044	Cervus elaphus scoticus mitochondrial...	50	2e-05
dbj AB021096.1 AB021096	Cervus elaphus canadensis mitochondrial...	50	2e-05
dbj AB021093.1 AB021093	Cervus nippon nippon mitochondrial ...	50	2e-05
dbj AB021090.1 AB021090	Cervus nippon pulchellus mitochondrial...	50	2e-05
dbj AB008535.1 AB008535	Dinodon semicarinatus mitochondrial...	50	2e-05
dbj AB006800.1 AB006800	Ovis aries mitochondrial DNA for cy...	50	2e-05
gb L12763.1 L0HMTCYTB	Lepidochelys kempi (Lk-3) mitochondrial...	50	2e-05
gb L08032.1 CPLMTCYTB	Carcharhinus plumbeus mitochondrial ...	50	2e-05
gb L28941.1 URRCYS	Uroderma bilobatum cytochrome b gene, 5'...	50	2e-05
gb L28937.1 CDECYB	Chiroderma doriae cytochrome b gene, 5' end	50	2e-05
emb AJ010056.1 CPY010056	Capra pyrenaica (individual 12) mit...	50	2e-05
emb AJ010054.1 CPY010054	Capra pyrenaica (individual 11) mit...	50	2e-05
emb AJ010053.1 CPY010053	Capra pyrenaica (individual 10) mit...	50	2e-05
emb AJ010052.1 CPY010052	Capra pyrenaica (individual 9) mit...	50	2e-05
emb AJ010051.1 CPY010051	Capra pyrenaica (individual 8) mit...	50	2e-05
emb AJ010050.1 CPY010050	Capra pyrenaica (individual 7) mit...	50	2e-05
emb AJ010049.1 CPY010049	Capra pyrenaica (individual 6) mit...	50	2e-05
emb AJ010048.1 CPY010048	Capra pyrenaica (individual 5) mit...	50	2e-05
emb AJ010047.1 CPY010047	Capra pyrenaica (individual 4) mit...	50	2e-05
emb X95777.1 CLMCE	C. longirostris mitochondrial cytochrome ...	50	2e-05
emb AJ009879.1 CIB9879	Capra ibex nubiana mitochondrial cyt...	50	2e-05
emb AJ010055.1 CIB010055	Capra ibex (individual 1) ibex mit...	50	2e-05
gb U08946.1 CAU08946	Coragyps atratus mitochondrial cytochr...	50	2e-05
gb U08945.1 CBU08945	Cathartes burrovianus mitochondrial cy...	50	2e-05
gb U08944.1 VGU08944	Vultur gryphus mitochondrial cytochrom...	50	2e-05
gb U08941.1 PAU08941	Platalea alba mitochondrial cytochrome ...	50	2e-05
gb U08940.1 PRU08940	Phoenicopterus ruber mitochondrial cyt...	50	2e-05
emb X95775.1 ACMCB	A. cristatus mitochondrial cytochrome b gene	50	2e-05
emb X95774.1 ABMCB	A. bennettii mitochondrial cytochrome b gene	50	2e-05
emb X95764.1 AAMCB	A. albertisi mitochondrial cytochrome b gene	50	8e-05
gb AF040383.1 AF040383	Alces alces cytochrome b (cytb) gene...	45	3e-04
gb AF232023.1 AF232023	Tamandua tetradactyla clone 7 cytoch...	45	3e-04
gb AF232022.1 AF232022	Tamandua tetradactyla clone 6 mitoch...	45	3e-04
gb AF232021.1 AF232021	Tamandua tetradactyla clone 5 cytoch...	45	3e-04
gb AF157466.1 AF157466	Lepus timidus cytochrome b (Cyb) gen...	45	3e-04
gb AF157465.1 AF157465	Lepus granatensis cytochrome b (Cyb) ...	45	3e-04
gb AF157464.1 AF157464	Lepus corsicanus haplotype 1 cytochr...	45	3e-04
gb AF157453.1 AF157463	Lepus corsicanus haplotype 3 cytochr...	45	3e-04
gb AF157460.1 AF157460	Lepus europaeus cytochrome b (Cyb) g...	45	3e-04
gb AF231664.1 AF231664	Tylosurus crocodilus crocodilus cyto...	45	3e-04
gb AF231663.1 AF231663	Tylosurus crocodilus clone STRI-1537...	45	3e-04
gb AF231662.1 AF231662	Tylosurus acus pacificus cytochrome ...	45	3e-04
gb AF231660.1 AF231660	Tylosurus acus melanotus clone STRI-...	45	3e-04
gb AF231659.1 AF231659	Tylosurus acus melanotus clone STRI-...	45	3e-04
gb AF231658.1 AF231658	Tylosurus acus imperialis cytochrome ...	45	3e-04
gb AF231657.1 AF231657	Tylosurus acus acus cytochrome b oxyd...	45	3e-04
gb AF231656.1 AF231656	Strongylura hubbsi cytochrome b oxid...	45	3e-04
gb AF231644.1 AF231644	Ablennes hians cytochrome b oxidase ...	45	3e-04
gb AF231639.1 AF231639	Tamandua tetradactyla clone 3 cytoch...	45	3e-04
gb AF232019.1 AF232019	Tamandua tetradactyla clone 1 cytoch...	45	3e-04
gb AF232017.1 AF232017	Mylodon darwini cytochrome b gene...	45	3e-04
gb AF232014.1 AF232014	Alligator mississippiensis isolate S...	45	3e-04
gb AFJ18564.1 AFJ18564	Alligator mississippiensis isolate S...	45	3e-04
gb AFJ18563.1 AFJ18563	Alligator mississippiensis isolate S...	45	3e-04
gb AFJ18562.1 AFJ18562	Alligator mississippiensis isolate G...	45	3e-04
gb AFJ18561.1 AFJ18561	Alligator mississippiensis isolate G...	45	3e-04
gb AFJ18560.1 AFJ18560	Alligator mississippiensis isolate A...	45	3e-04
gb AFJ18559.1 AFJ18559	Alligator mississippiensis isolate A...	45	3e-04
gb AFJ18558.1 AFJ18558	Alligator mississippiensis isolate S...	45	3e-04
gb AFJ18557.1 AFJ18557	Alligator mississippiensis isolate S...	45	3e-04
gb AFJ18556.1 AFJ18556	Alligator mississippiensis isolate S...	45	3e-04
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gb AFJ18554.1 AFJ18554	Alligator mississippiensis isolate S...	45	3e-04
gb AFJ18553.1 AFJ18553	Alligator mississippiensis isolate L...	45	3e-04
gb AFJ18552.1 AFJ18552	Alligator mississippiensis isolate L...	45	3e-04
gb AFJ18551.1 AFJ18551	Alligator mississippiensis isolate L...	45	3e-04
gb AFJ18550.1 AFJ18550	Alligator mississippiensis isolate F...	45	3e-04
gb AFJ18549.1 AFJ18549	Alligator mississippiensis isolate F...	45	3e-04
gb AFJ18548.1 AFJ18548	Alligator mississippiensis isolate F...	45	3e-04
gb AFJ18041.1 AFJ18041	Sorex monticolus specimen-voucher AF...	45	3e-04

<u>gb AF326272.1 AF326272</u>	Myospalax myospalax cytochrome b (cy... gb AF326271.1 AF326271	Myospalax psilurus isolate 2 cytochr... gb AF326270.1 AF326270	Myospalax psilurus isolate 1 cytochr... gb AF326266.1 AF326266	Eospalax fontanieri isolate 4 cytoc... emb AJ004340.1 ADAJ4340	Acrocephalus dumetorum mitochondria... emb AJ004264.1 ADAJ4264	Acrocephalus dumetorum mitochondria...
						.46 3e-04
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						.46 3e-04
						.44 0.001
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Alignments

<u>tmpseq_0</u>	1	taccatgaggacaaatattcatcccg	25
<u>AF231651</u>	398	422
<u>AF231650</u>	398	422
<u>NC_002672</u>	15560	15584
<u>NC_002673</u>	15552	15576
<u>AF232015</u>	398	422
<u>AF232013</u>	398	422
<u>AY016015</u>	15552	15576
<u>AY016013</u>	15560	15584
<u>AY016014</u>	11516	11540
<u>AF230167</u>	266	290
<u>AF074594</u>	206	230
<u>AY005210</u>	290	314
<u>AY005209</u>	290	314
<u>AY005208</u>	290	314
<u>AY005205</u>	290	314
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<u>AF243857</u>	275	299
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Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885

Number of sequences in database: 807,597

Lambda K H
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Gapped
Lambda K H
1.37 0.711 1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 39355

Number of Sequences: 807597

Number of extensions: 39355

Number of successful extensions: 15066

Number of sequences better than 10.0: 5706

length of query: 25

length of database: 2,863,827,885

effective HSP length: 17

effective length of query: 8

effective length of database: 2,850,098,736

effective search space: 22800789888

effective search space used: 22800789888

T: 0

A: 30

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 16 (32.2 bits)

Table 11. BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593033-24247-14777

Query-

(26 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQ's

Taxonomy reports

Distribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

		Score (bits)	E Value
gb AF189111.1 AF189111	Cryptotermes austrinus cytochrome b ...	52	6e-06
gb U86834.1 U86834	Phyllotis wolffsohni MSA 67270 cytochrom...	52	6e-06
gb AF123633.1 AF123633	Perissoccephalus tricolor cytochrome ...	52	6e-06
gb AF123617.1 AF123617	Pipreola acutata cytochrome b gene, ...	52	6e-06
gb AF127202.1 AF127202	Hyloperusz fulviventris cytochrome b ...	52	6e-06
gb AF127194.1 AF127194	Grallaria guatimalensis cytochrome b...	52	6e-06
gb AF217828.1 AF217828	Aspidelaps scutatus cytochrome b gen...	52	6e-06
gb AF160578.1 AF160578	Hypogeomys antimena Mant555 cytochro...	52	6e-06
gb AF009931.2 AF009931	Archocentrus centrarchus cytochrome ...	52	6e-06
gb AF091629.1 AF091629	Antilocapra americana cytochrome b (...)	52	6e-06
gb AF034967.1	Sigmodon lichtensteinii cytochrome b gene, ...	52	6e-06
gb AF038290.1 AF038290	Antechinus sp. cytochrome b gene, mi...	52	6e-06
gb U07577.1 AMU07577	Antechinus melanurus mitochondrial cyt...	52	6e-06
gb U81343.1 CFU81343	Chelus fimbriata cytochrome b gene, mi...	52	6e-06
emb AJ222681.1 ABCYTB8	Alcelaphus buselaphus mitochondrial ...	52	6e-06
gb M99464.1 PNZMTCYT8	Planigale sp. cytochrome b gene, comp...	52	6e-06
emb AJ225116.1 DNJ225116	Dryomys nitedula mitochondrial gen...	52	6e-06
gb U25738.1 PRU25738	Paradisaea raggiana cytochrome b gene, ...	52	6e-06
gb U25736.1 PRU25736	Paradisaea rubra cytochrome b gene, mi...	52	6e-06
gb U15202.1 SMU15202	Seleucidis melanoleuca mitochondrial c...	52	6e-06
gb U15204.1 PR15204	Paradisaea raggiana mitochondrial cytoc...	52	6e-06
emb X56290.1 MIDDCYT8	D.dama mitochondrion cyt b gene for cy...	52	6e-06
emb XS6286.1 MIAACYTB8	A.americana mitochondrion cyt b gene ...	52	6e-06
dbj D88639.1 D88639	Anoa depressicornis mitochondrial DNA f...	52	6e-06
dbj D82890.1 D82890	Bubalus depressicornis mitochondrial DN...	52	6e-06
gb AF119261.1 AF119261	Peromyscus maniculatus cytochrome b ...	45	3e-04
gb AF123615.1 AF123615	Rupicola rupicola cytochrome b gene, ...	45	3e-04
gb AF160603.1 AF160603	Apodemus sylvaticus Asyl588 cytochro...	45	3e-04
gb U62687.1 CCOLCYTB2	Charadrius collaris cytochrome b (cyt...)	45	3e-04
gb U62685.1 CBICCYTB2	Charadrius bicinctus cytochrome b (cyt...)	45	3e-04
gb AF022071.1	Madoqua guentheri cytochrome b (cytb) gene, ...	45	3e-04
gb AF022070.1	Madoqua kirkii cytochrome b (cytb) gene, mit...	45	3e-04
gb U81317.1 PSU83317	Poliherax semitorquatus cytochrome b ...	45	3e-04
gb U37293.1 CCU37293	Cephus columba cytochrome b gene, mit...	45	3e-04
gb U37292.1 CCU37292	Cephus carbo cytochrome b gene, mitoc...	45	3e-04
gb U37291.1 BMU37291	Brachyrhampus marmoratus perdix cytoch...	45	3e-04
gb AF082055.1 AF082055	Rupicola rupicola cytochrome b gene, ...	45	3e-04
gb U72770.1 JMU72770	Jabiru mycteria cytochrome b gene, mit...	45	3e-04
gb U07578.1 DCU07578	Dasyercuscristicauda mitochondrion c...	45	3e-04
gb AF031908.1 GOCCCYT8	Geopsittacus occidentalis cytochrom...	45	3e-04
emb AJ004231.1 SBAJ4231	Sula bassana mitochondrial cyt b gen...	45	3e-04
emb AJ004230.1 SBAJ4230	Sula bassana mitochondrial cyt b gen...	45	3e-04
emb AJ004229.1 SBAJ4229	Sula bassana mitochondrial cyt b gen...	45	3e-04
emb AJ004232.1 SBAJ4232	Sula bassana mitochondrial cyt b gen...	45	3e-04
gb U88865.1	Pomacentrus sp. cytochrome b (cytb) gene, mito...	45	3e-04
gb U90001.1 MBU90001	Morus bassanus cytochrome b gene, mito...	45	3e-04
gb U63057.1 BMU63057	Brachyrhampus marmoratus perdix cytoch...	45	3e-04
dbj AB036404.1 AB036404	Rana porosa brevipoda mitochondrial...	45	3e-04
dbj AB036402.1 AB036402	Rana porosa brevipoda mitochondrial...	45	3e-04
dbj AB036400.1 AB036400	Rana porosa brevipoda mitochondrial...	45	3e-04
dbj AB036398.1 AB036398	Rana porosa porosa mitochondrial CN...	45	3e-04
gb U19611.1 JMU19611	Jabiru mycteria cytochrome b gene, mit...	45	3e-04
emb X92519.1 MACYTB	H.ampullatus cytochrome b gene (complet...	45	3e-04
gb L08014.1 GAENTCCTB8	Galeocerdo cuvier mitochondrial cyto...	45	3e-04
gb L08031.1 CPMLCYTB8	Carcharhinus porosus mitochondrial c...	45	3e-04
gb AY015012.1	Crypturellus tacaupa mitochondrial, partial ...	44	0.001
gb AF074591.1 AF074591	Petrochelidon pyrrhonota cytochrome ...	44	0.001
gb AY005212.1	Pooospiza whitii isolate 2 cytochrome b (cytb...)	44	0.001
gb AY005211.1	Pooospiza whitii isolate 1 cytochrome b (cytb...)	44	0.001
gb AF189122.1 AF189122	Cryptotermes tropicalis cytochrome b ...	44	0.001
gb AF189120.1 AF189120	Cryptotermes secundus cytochrome b (...)	44	0.001
gb AF189119.1 AF189119	Cryptotermes primus isolate 2 cytoch...	44	0.001
gb AF189117.1 AF189117	Cryptotermes primus isolate 1 cytoch...	44	0.001
gb AF189116.1 AF189116	Cryptotermes dudleyi cytochrome b (Cy...)	44	0.001
gb AF189114.1 AF189114	Ovula canadensis cytochrome b gene, p ...	44	0.001
gb AF189112.1 AF189112	Ovula canadensis canadensis cytochro...	44	0.001
gb AF189110.1 AF189110	Ovula canadensis neleoni cytochrome b ...	44	0.001
gb AF222681.1 AF222681	Vireo cassinii cassinii specimen-vnu	44	0.001

gb AF081989.1 AF081989	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081988.1 AF081988	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081987.1 AF081987	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081986.1 AF081986	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081985.1 AF081985	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081984.1 AF081984	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081983.1 AF081983	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081982.1 AF081982	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081981.1 AF081981	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081980.1 AF081980	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081979.1 AF081979	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081978.1 AF081978	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081977.1 AF081977	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081976.1 AF081976	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081975.1 AF081975	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081974.1 AF081974	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081973.1 AF081973	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081972.1 AF081972	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081971.1 AF081971	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081970.1 AF081970	Vireo solitarius alticola country US...	44	0.001
gb AF081969.1 AF081969	Vireo solitarius alticola country US...	44	0.001
gb AF081968.1 AF081968	Vireo solitarius alticola country US...	44	0.001
gb AF081967.1 AF081967	Vireo solitarius alticola country US...	44	0.001
gb AF081966.1 AF081966	Vireo solitarius solitarius specimen...	44	0.001
gb AF081965.1 AF081965	Vireo solitarius solitarius specimen...	44	0.001
gb AF081964.1 AF081964	Vireo solitarius solitarius specimen...	44	0.001
gb AF081962.1 AF081962	Vireo flavifrons specimen-voucher LS...	44	0.001
gb AF081961.1 AF081961	Vireo flavifrons specimen-voucher LS...	44	0.001
gb AF081960.1 AF081960	Vireo leucophrys leucophrys specimen...	44	0.001
gb AF081959.1 AF081959	Vireolanius leucotis leucotis cytoch...	44	0.001
gb AF112405.2 AF112405	Barbus anoplus cytochrome b (cytb) g...	44	0.001
gb AF144317.1 AF144317	Amphiprion ocellaris isolate 3 haplo...	44	0.001
gb AF144316.1 AF144316	Amphiprion ocellaris haplotype 3DH11...	44	0.001
gb AF144315.1 AF144315	Amphiprion ocellaris haplotype 3DH15...	44	0.001
gb AF144314.1 AF144314	Amphiprion ocellaris isolate 2 haplo...	44	0.001
gb AF144313.1 AF144313	Amphiprion ocellaris isolate 1 haplo...	44	0.001
gb AF144312.1 AF144312	Amphiprion ocellaris haplotype 3DH12...	44	0.001
gb AF144311.1 AF144311	Amphiprion ocellaris haplotype 3DH1 ...	44	0.001
gb AF144310.1 AF144310	Amphiprion ocellaris isolate 2 haplo...	44	0.001
gb AF144309.1 AF144309	Amphiprion ocellaris isolate 1 haplo...	44	0.001
ref NC_001567.1 Bos taurus mitochondrion, complete genome		44	0.001
gb AF212124.1 AF212124	Anolis schwartzii cytochrome b gene...	44	0.001
gb AF182706.1 AF182706	Phapitreron amethystina cytochrome b...	44	0.001
gb AF010406.1 AF010406	Ovis aries complete mitochondrial ge...	44	0.001
gb AF096452.1 AF096452	Platysteira cyanea cytochrome b gene...	44	0.001
gb AF283619.1 AF283619	Elaphe obsoleta LSUMZ J9162 cytochrom...	44	0.001
gb AF283618.1 AF283618	Elaphe obsoleta LSUMZ H15896 cytochr...	44	0.001
gb AF283608.1 AF283608	Elaphe obsoleta LSUMZ H14782 cytochr...	44	0.001
gb AF283602.1 AF283602	Elaphe obsoleta LSUMZ H3388 cytochro...	44	0.001
gb AFJ10069.1 AFJ10069	Elaenia martinica cytochrome b gene...	44	0.001
gb AF146616.1 AF146616	Actophilornis africanus cytochrome b...	44	0.001
gb AF271410.1 AF271410	Galago moholi cytochrome b (cyt b) g...	44	0.001
gb AF290139.1 AF290139	Peucedramus taeniatus cytochrome b (...)	44	0.001
ref NC_002504.1 Lama pacos mitochondrion, complete genome		44	0.001
gb AF163901.1 AF163901	Microtus ochrogaster cytochrome b ge...	44	0.001
gb AF119263.1 AF119263	Myopus schisticolor cytochrome b gen...	44	0.001
gb AF119259.1 AF119259	Synaptomyia borealis cytochrome b gen...	44	0.001
gb AF288454.1 AF288454	Nyctereutes procyonoides koreensis c...	44	0.001
gb AF153895.1 AF153895	Microtus gregalis cytochrome B (cytB...)	44	0.001
gb AF123649.1 AF123649	Machaeropterus regulus acrolatus cy...	44	0.001
gb AF123647.1 AF123647	Machaeropterus pyrocephalus cytochro...	44	0.001
gb AF123646.1 AF123646	Xenopipo attonitens cytochrome b gen...	44	0.001
gb AF123645.1 AF123645	Pipra fasciicauda cytochrome b gene...	44	0.001
gb AF123644.1 AF123644	Pyroderces ecuatus cytochrome b gene...	44	0.001
gb AF123633.1 AF123633	Cephalopterus ornatus cytochrome b g...	44	0.001
gb AF123628.1 AF123628	Turdampallicryptoleucus cytochrome ...	44	0.001
gb AF123621.1 AF123621	Porphyrolaema porphyrolaema cytochro...	44	0.001
gb AF123619.1 AF123619	Amphilophus tequendama cytochrome b g...	44	0.001
gb AF123618.1 AF123618	Pipreola chlorolepidota cytochrome b...	44	0.001
gb AF123617.1 AF123617	Rupicola peruviana cytochrome b geno...	44	0.001
gb AF123616.1 AF123616	Dolichonyx oryzivorus cytochrome b geno...	44	0.001

gb AF127201.1 AF127201	Myrmothera campanisona cytochrome b ...	44	0.001
gb AF127192.1 AF127192	Grallaria ruficapilla cytochrome b g...	44	0.001
gb AF127189.1 AF127189	Grallaria varia cytochrome b gene, p...	44	0.001
gb AF197849.1 AF197849	Sericornis frontalis cytochrome b ge...	44	0.001
gb AF197847.1 AF197847	Pardalotus striatus cytochrome b gen...	44	0.001
ref NC_000889.1	Hippopotamus amphibius mitochondrion, comp...	44	0.001
ref NC_002079.1	Carassius auratus mitochondrion, complete ...	44	0.001
ref NC_001794.1	Macropus robustus mitochondrion, complete ...	44	0.001
ref NC_001610.1	Didelphis virginiana mitochondrion, comple...	44	0.001
gb AF201612.1 AF201612	Stomatochimus sp. CU79703 cytochrome...	44	0.001
gb AF097931.1 AF097931	Amphiprion clarkii cytochrome b gene...	44	0.001
gb AF097927.1 AF097927	Amphiprion ocellaris cytochrome b ge...	44	0.001
gb J01394.1 BOVMT_Bos taurus	taurus mitochondrion, complete genome	44	0.001
gb AF168760.1 AF168760	Agalone spinifera isolate TXsc cytoc...	44	0.001
gb AF168759.1 AF168759	Agalone spinifera isolate TXki cytoc...	44	0.001
gb AF168758.1 AF168758	Agalone spinifera isolate TXcc cytoc...	44	0.001
gb AF168756.1 AF168756	Agalone spinifera isolate NMrg cytoc...	44	0.001
gb AF182381.1 AF182381	Petrochelidon rufof collaris isolate E...	44	0.001
gb AF182380.1 AF182380	Petrochelidon rufof collaris isolate E...	44	0.001
gb U89187.1 MMU89187	Memotus mexicanus cytochrome b (cytb) ...	44	0.001
gb AF193833.1 AF193833	Botaurus lentiginosus cytochrome b g...	44	0.001
gb AF193822.1 AF193822	Ardea alba cytochrome b gene, partia...	44	0.001
gb AF193821.1 AF193821	Ardea herodias cytochrome b gene, pa...	44	0.001
gb AF217837.1 AF217837	Paranaja multifasciata cytochrome b ...	44	0.001
gb AF217835.1 AF217835	Naja kaouthia cytochrome b gene, com...	44	0.001
gb AF217834.1 AF217834	Laticauda colubrina cytochrome b gen...	44	0.001
gb AF217831.1 AF217831	Calliophis japonicus cytochrome b ge...	44	0.001
gb AF217823.1 AF217823	Micruroides euryxanthus cytochrome b...	44	0.001
gb AF217819.1 AF217819	Drysdalia coronata cytochrome b gene...	44	0.001
gb AF217815.1 AF217815	Austrelaps superbus cytochrome b gen...	44	0.001
gb AF118156.1 AF118156	Terenura humeralis specimen-voucher ...	44	0.001
gb AF209938.1 AF209938	Euura atra isolate 62 cytochrome b g...	44	0.001
gb AF209933.1 AF209933	Euura atra isolate C cytochrome b ge...	44	0.001
gb AF059104.1 AF059104	Marmaronetta angustirostris cytochro...	44	0.001
gb AF059102.1 AF059102	Lophonetta specularoides cytochrome ...	44	0.001
gb AF059054.1 AF059054	Amazonetta brasiliensis cytochrome b...	44	0.001
gb AF192646.1 AF192646	Hippocampus barbouri haplotype PH.22...	44	0.001
gb AF192645.1 AF192645	Hippocampus barbouri haplotype PH.13...	44	0.001
gb AF160614.1 AF160614	Cricetomys gambianus CgAm518 cytochr...	44	0.001
gb AF160613.1 AF160613	Cricetomys emini Cemi511 cytochrome ...	44	0.001
gb AF160612.1 AF160612	Cricetomys emini Cemi530 cytochrome ...	44	0.001
gb AF160611.1 AF160611	Cricetomys emini Cemi537 cytochrome ...	44	0.001
gb AF160610.1 AF160610	Cricetomys emini Cemi636 cytochrome ...	44	0.001
gb AF160604.1 AF160604	Calomyscus bailwardi Cbal576 cytochr...	44	0.001
gb AF160560.1 AF160560	Eliurus majori Emaj642 cytochrome b ...	44	0.001
gb AF160559.1 AF160559	Eliurus majori Emaj641 cytochrome b ...	44	0.001
gb AF160558.1 AF160558	Eliurus majori Emaj639 cytochrome b ...	44	0.001
gb AF160557.1 AF160557	Eliurus majori Emaj638 cytochrome b ...	44	0.001
gb AF160555.1 AF160555	Eliurus majori Emaj614 cytochrome b ...	44	0.001
gb AF160554.1 AF160554	Eliurus majori Emaj617 cytochrome b ...	44	0.001
gb AF160553.1 AF160553	Eliurus majori Emaj573 cytochrome b ...	44	0.001
gb AF160552.1 AF160552	Eliurus majori Emaj556 cytochrome b ...	44	0.001
gb AF160551.1 AF160551	Eliurus majori Emaj561 cytochrome b ...	44	0.001
gb AF160550.1 AF160550	Eliurus majori Emaj443 cytochrome b ...	44	0.001
gb AF160549.1 AF160549	Eliurus majori Emaj444 cytochrome b ...	44	0.001
gb AF016287.1 AF016287	Damaliscus pygargus cytochrome b (cy...)	44	0.001
gb AF016286.1 AF016286	Oryx leucoryx cytochrome b (cytb) ge...	44	0.001
gb AF016283.1 AF016283	Antilope cervicapra cytochrome b (cy...)	44	0.001
gb AF016281.1 AF016281	Antidorcas maculipennis cytochrome b ...	44	0.001
gb AF016278.1 AF016278	Tragelaphus oryx cytochrome b (cytb) ...	44	0.001
gb AF016276.1 AF016276	Tragelaphus euryceros cytochrome b (...	44	0.001
gb AF015274.1	Tetracerus quadricornis cytochrome b (cytb) ...	44	0.001
ref NC_001941.1	Ovis aries mitochondrion, complete genome	44	0.001
gb AF109698.1 AF109698	Microcyzomyia minutus cytochrome 8 (c...	44	0.001
gb AF109692.1 AF109692	Rhipidomyia nitela cytochrome 8 (cytB...)	44	0.001
gb AF109671.1 AF109671	Thomasomyia daphne cytochrome 8 (cytB...)	44	0.001
gb AF109652.1 AF109652	Scapteromyia tumidae cytochrome 8 (cy...	44	0.001
gb AF012720.1 AF012720	Magemuntiacus vuquangensis cytochrom...	44	0.001
gb AF012719.1	Muntiacus muntjak cytochrome b gene, mitocho...	44	0.001
gb AF022199.1 AF022199	Stenelle coeruleoalba cytochrome b g...	44	0.001
gb AF022199.1 AF022199	Stenelle coeruleoalba cytochrome b g ...	44	0.001

gb AF084074.1 AF084074	Lagenorhynchus albostriatus cytochrome...	44	0.001
gb AF090750.1 AF090750	Gobio gobio balcanicus cytochrome b ...	44	0.001
gb AF157939.1 AF157939	Spermophilus columbianus columbianus...	44	0.001
gb AF157937.1 AF157937	Spermophilus washingtoni isolate S89...	44	0.001
gb AF157936.1 AF157936	Spermophilus washingtoni isolate S88...	44	0.001
gb AF157915.1 AF157915	Spermophilus richardsoni isolate S63...	44	0.001
gb AF157914.1 AF157914	Spermophilus richardsoni isolate S62...	44	0.001
gb AF157912.1 AF157912	Spermophilus undulatus isolate S60 c...	44	0.001
gb AF157906.1 AF157906	Spermophilus undulatus isolate S55 c...	44	0.001
gb AF157891.1 AF157891	Spermophilus elegans elegans isolate...	44	0.001
gb AF157882.1 AF157882	Spermophilus columbianus columbianus...	44	0.001
gb AF157859.1 AF157859	Spermophilus citellus isolate S118 c...	44	0.001
gb AF157858.1 AF157858	Spermophilus citellus isolate S117 c...	44	0.001
gb AF157839.1 AF157839	Spermophilus elegans elegans isolate...	44	0.001
gb AF030497.1 AF030497	Crocidura brunnea cytochrome b (cyt ...	44	0.001
gb U03541.2 LAU03541	Lenoxus apicalis cytochrome b gene, pa...	44	0.001
gb AF009951.2 AF009951	Heros appendiculatus cytochrome b (c...	44	0.001
gb AF009941.1 AF009941	Tomocichla tuba cytochrome b (cytb) ...	44	0.001
gb AF009925.1 AF009925	Archocentrus sajica cytochrome b (cy...	44	0.001
cb AF094633.1 AF094633	Stachyris whiteheadi cytochrome b ge...	44	0.001
cb AF094621.1 AF094621	Eminia lepida cytochrome b gene, par...	44	0.001
gb AF094618.1 AF094618	Hypergerus atriceps cytochrome b gen...	44	0.001
gb AF166348.1 AF166348	Phascolarctos cinereus cytochrome b ...	44	0.001
gb AF158697.1 AF158697	Geomys bursarius ozarkensis cytochro...	44	0.001
gb AF158694.1 AF158694	Geomys bursarius majusculus cytochro...	44	0.001
gb AF158693.1 AF158693	Geomys bursarius bursarius cytochrom...	44	0.001
gb AF158688.1 AF158688	Geomys bursarius missouriensis cytoc...	44	0.001
gb AF100720.1 AF100720	Spermophilus citellus cytochrome b (...)	44	0.001
cb AF091632.1 AF091632	Bubalus depressicornis cytochrome b ...	44	0.001
gb AF102815.1 AF102815	Dromiciops gliroides cytochrome b ge...	44	0.001
gb AF102814.1 AF102814	Vombatus ursinus cytochrome b gene, ...	44	0.001
gb AF022065.1	Tragelaphus euryceus cytochrome b (cytb) ge...	44	0.001
gb AF022059.1	Kobus ellipsiprymnus cytochrome b (cytb) gen...	44	0.001
gb AF022058.1	Antilope cervicapra cytochrome b (cytb) gene...	44	0.001
gb AF022057.1	Tragelaphus oryx cytochrome b (cytb) gene, m...	44	0.001
gb AF022054.1	Antidorcas marsupialis cytochrome b (cytb) g...	44	0.001
gb AF016637.1 AF016637	Connochaetes gnou cytochrome b (cytb...)	44	0.001
gb U69863.1 PSU69863	Python sebae cytochrome b (cytb) gene,...	44	0.001
gb U69844.1 LTU69844	Lichenura trivirgata cytochrome b (cyt...	44	0.001
gb AF143193.1 AF143193	Epinephelus sp. cytochrome b (cytb) ...	44	0.001
gb AF121222.1 AF121222	Amphiprion ocellaris isolate 8 cytoc...	44	0.001
gb AF096625.1 AF096625	Kobus ellipsiprymnus defassa cytochr...	44	0.001
gb AF096624.1 AF096624	Kobus ellipsiprymnus ellipsiprymnus c...	44	0.001
gb AF081052.1 AF081052	Eulemur rubriventer cytochrome b (cy...	44	0.001
gb AF081049.1 AF081049	Eulemur macaco macaco cytochrome b (...)	44	0.001
gb AF081048.1 AF081048	Eulemur fulvus albifrons cytochrome ...	44	0.001
gb AF082063.1 AF082063	Elminia longicauda cytochrome b gene...	44	0.001
emb AJ010957.1 HAAJ10957	Hippopotamus amphibius complete mi...	44	0.001
gb U76506.1 CLU76506	Chlamydera lauterbachii cytochrome b g...	44	0.001
gb U76504.1 CCU76504	Chlamydera cerviniventris cytochrome b...	44	0.001
gb U76505.1 ASU76505	Amblyornis subalaris cytochrome b gene...	44	0.001
gb U76503.1 APU76503	Archboldia papuensis cytochrome b gene...	44	0.001
gb U76508.1 AIU76508	Amblyornis inornatus cytochrome b gene...	44	0.001
gb AF034969.1 AF034969	Connochaetes taurinus cytochrome b g...	44	0.001
gb AF051875.1 AF051875	Rhodeus ocellatus cytochrome b (cytb...)	44	0.001
gb AF082007.1 AF082007	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082005.1 AF082005	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082004.1 AF082004	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082003.1 AF082003	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082002.1 AF082002	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF092001.1 AF092001	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF092000.1 AF092000	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF091999.1 AF091999	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF091998.1 AF091998	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF091227.1 AF091227	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF091996.1 AF091996	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF091225.1 AF091225	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF091224.1 AF091224	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF091223.1 AF091223	Vireo plumbeus plumbeus specimen-vou...	44	0.001

gb AF081991.1 AF081991	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb S73150.1 S73150	cytochrome b (<i>Spermophilus richardsonii</i>)...	44	0.001
gb AF012235.1 AF012235	Cryptomys hottentotus natalensis cyt...	44	0.001
gb US3580.1 NCUS3580	<i>Nycticebus coucang</i> cytochrome b (cyt b...)	44	0.001
gb US3577.1 EFUS3577	<i>Eulemur fulvus rufus</i> cytochrome b (cyt...)	44	0.001
gb US3576.1 EFUS3576	<i>Eulemur fulvus collaris</i> cytochrome b (...)	44	0.001
gb U95512.1 ESERCYTB2	<i>Eptesicus serotinus</i> 3' cytochrome b (...)	44	0.001
gb U95508.1 PKUHLCYTB2	<i>Pipistrellus kuhli</i> 5' cytochrome b (...)	44	0.001
gb U17863.1 BTU17868	<i>Budorcas taxicolor taxicolor</i> cytochrom...	44	0.001
gb U17867.1 BTU17867	<i>Budorcas taxicolor bedfordi</i> cytochrome...	44	0.001
gb U17860.1 ODU17860	<i>Ovis dalli</i> cytochrome b gene, mitochon...	44	0.001
gb U17859.1 OCU17859	<i>Ovis canadensis</i> cytochrome b gene, mit...	44	0.001
emb AJ010556.1 ASPO10556	<i>Acomys spinosissimus</i> mitochondrial...	44	0.001
gb AF034736.1 AF034736	<i>Capra falconeri</i> cytochrome b (cytb) ...	44	0.001
gb AF034730.1 AF034730	<i>Ovis aries</i> cytochrome b (cytb) gene, ...	44	0.001
gb AF034729.1 AF034729	<i>Ovis vignei</i> cytochrome b (cytb) gene...	44	0.001
gb AF034728.1	<i>Ovis dalli dalli</i> cytochrome b (cytb) gene, m...	44	0.001
gb AF034727.1	<i>Ovis ammon darwini</i> cytochrome b (cytb) gene, ...	44	0.001
gb AF034724.1 AF034724	<i>Pantholops hodgsoni</i> cytochrome b (cy...	44	0.001
gb AF034722.1 AF034722	<i>Addax nasomaculatus</i> cytochrome b (cy...	44	0.001
gb U72038.1 MMU72038	<i>Monodon monoceros</i> cytochrome b (cytb), ...	44	0.001
gb U72037.1 DLU72037	<i>Delphinapterus leucas</i> cytochrome b (cy...	44	0.001
gb M99455.1 M99455CYTB	<i>Murexia longicaudata</i> cytochrome b gen...	44	0.001
gb L29055.1 SKPMTDLOOP	Sheep mitochondrial cytochrome b (Cy...)	44	0.001
gb AF082047.1 AF082047	<i>Coccyzus americanus</i> cytochrome b gen...	44	0.001
gb AF038286.1 AF038286	<i>Antechinus minimus</i> cytochrome b gene...	44	0.001
gb AF038284.1 AF038284	<i>Antechinus swainsonii</i> cytochrome b g...	44	0.001
gb AF059093.1 AF059093	<i>Anas undulata</i> cytochrome b gene, par...	44	0.001
gb AF059092.1 AF059092	<i>Anas superciliosa rogersi</i> cytochrome...	44	0.001
gb AF059091.1 AF059091	<i>Anas sparsa</i> cytochrome b gene, parti...	44	0.001
gb AF059080.1 AF059080	<i>Anas melleri</i> cytochrome b gene, part...	44	0.001
gb AF059078.1 AF059078	<i>Anas laysanensis</i> cytochrome b gene, ...	44	0.001
gb AF052240.1 AF052240	<i>Anairetes flavirostris</i> cytochrome b ...	44	0.001
gb AF006240.1 AF006240	<i>Mitrospingus cassinii</i> cytochrome b (...)	44	0.001
gb AF006227.1 AF006227	<i>Dacnis cayana</i> cytochrome b (cytb) ge...	44	0.001
gb AF047447.1 AF047447	<i>Oryx leucoryx</i> cytochrome b gene, mit...	44	0.001
gb U07576.1 AHU07576	<i>Antechinus habbema</i> mitochondrial cytoc...	44	0.001
gb AF028180.1 AF028180	<i>Urocyon cinereoargenteus</i> cytochrome ...	44	0.001
gb AF028178.1 AF028178	<i>Pseudalopex sechurae</i> cytochrome b (c...	44	0.001
gb AF028170.1 AF028170	<i>Vulpes zerda</i> cytochrome b (cytb) gen...	44	0.001
gb M99454.1 ASWMTSCYTB	<i>Antechinus stuartii</i> cytochrome b gen...	44	0.001
gb M99453.1 ASWMTSCYTB	<i>Antechinus swainsonii</i> cytochrome b ge...	44	0.001
gb U23461.1 ANU23461	<i>Antechinus naso</i> cytochrome b gene, mit...	44	0.001
gb U87138.1 TVU87138	<i>Trichosurus vulpecula</i> cytochrome b (cy...	44	0.001
gb U07590.1 PMU07590	<i>Planigale maculata</i> mitochondrial cytoc...	44	0.001
emb AJ004326.1 PTAJ4326	<i>Phylloscopus trochilus</i> mitochondria...	44	0.001
gb AF020255.1 AF020255	<i>Cyclura nubila</i> cytochrome b (cytb) g...	44	0.001
emb Y19184.1 LPA19184	Lama pacos complete mitochondrial genome	44	0.001
gb U88862.1	<i>Amphilophus citrinellum</i> cytochrome b (cytb) ge...	44	0.001
gb U88859.1	<i>Thorichthys aureum</i> cytochrome b (cytb) gene, m...	44	0.001
gb U88858.1	<i>Thorichthys cf. aureum</i> cytochrome b (cytb) gen...	44	0.001
gb U88857.1	<i>Herichthys labridens</i> cytochrome b (cytb) gene, ...	44	0.001
gb U88856.1	<i>Herichthys carpintis</i> cytochrome b (cytb) gene, ...	44	0.001
emb Y10524.1 MIMRCEN	<i>Macropus robustus</i> complete mitochondrial...	44	0.001
gb U81357.1 CSU81357	<i>Chelydra serpentina</i> cytochrome b gene...	44	0.001
gb U81356.1 CLU81356	<i>Chelodina longicollis</i> cytochrome b gen...	44	0.001
gb U75534.1 LUU75534	<i>Leptomyrmex unicolor</i> cytochrome b gene...	44	0.001
gb U77332.1 GCU77332	<i>Gymnorhinus cyanocephala</i> cytochrome-b ...	44	0.001
emb Z29571.1 DMVMTGNME	<i>Didelphis virginiana</i> complete mitocho...	44	0.001
emb AJ222679.1 BTCTYTOP	<i>Boselaphus tragocamelus</i> mitochondria...	44	0.001
emb AJ222680.1 TSCYTOP	<i>Tragelaphus spekii</i> mitochondrial cyt...	44	0.001
emb AJ222683.1 ODCTOB	Oryx dammah mitochondrial cytochrome...	44	0.001
gb M29456.1 PMLMTCYTB	<i>Perameles nasuta</i> cytochrome b gene, C...	44	0.001
gb M29457.1 THNMTSCYTB	<i>Thylacinus cynocephalus</i> cytochrome b...	44	0.001
gb M29450.1 DAVMTCYTB	<i>Oscynurus hallucatus</i> cytochrome b gene...	44	0.001
gb U23717.1 PMU23717	<i>Paradiasea minor</i> cytochrome b gene, mi...	44	0.001
gb U15301.1 PRU15301	<i>Paradiasea rudolphi</i> mitochondrial cyto...	44	0.001
gb U15203.1 EAU15203	<i>Epinomachus albisetosus</i> mitochondrial cyto...	44	0.001
gb U15200.1 DRU15200	<i>Diphyllodes reproductus</i> mitochondrial C...	44	0.001
emb J99474.1 STAY174	<i>Sorex tundrenensis</i> parcell mitochondrial...	44	0.001
emb A899121.1 STAY121	<i>Sorex tundrenensis</i> parcell mitochondrial...	44	0.001

<u>emb</u>	<u>AJ000438.1</u>	<u>SIAJ438</u>	Sorex isodon partial mitochondrial c...	44	0.001
<u>emb</u>	<u>AJ000437.1</u>	<u>SIAJ437</u>	Sorex isodon partial mitochondrial c...	44	0.001
<u>emb</u>	<u>AJ000428.1</u>	<u>SAAJ428</u>	Sorex arcticus partial mitochondrial...	44	0.001
<u>emb</u>	<u>AJ000427.1</u>	<u>SAAJ427</u>	Sorex arcticus ssp. maritimensis par...	44	0.001
<u>emb</u>	<u>AJ000426.1</u>	<u>SAAJ426</u>	Sorex asper partial mitochondrial cy...	44	0.001
<u>emb</u>	<u>AJ000425.1</u>	<u>SAAJ425</u>	Sorex asper partial mitochondrial cy...	44	0.001
<u>emb</u>	<u>AJ000418.1</u>	<u>SGAJ418</u>	Sorex granarius partial mitochondria...	44	0.001
<u>emb</u>	<u>AJ000417.1</u>	<u>SGAJ417</u>	Sorex granarius partial mitochondria...	44	0.001
<u>emb</u>	<u>AJ000416.1</u>	<u>SAAJ416</u>	Sorex araneus partial mitochondrial ...	44	0.001
<u>emb</u>	<u>AJ004793.1</u>	<u>HCAJ4793</u>	Hippolais caligata ssp. caligata mi...	44	0.001
<u>emb</u>	<u>AJ004792.1</u>	<u>HCAJ4792</u>	Hippolais caligata ssp. rama mitoch...	44	0.001
<u>gb</u>	<u>U15718.1</u>	<u>RSU15718</u>	Ramphocelus sanguinolentus cytochrome ...	44	0.001
<u>gb</u>	<u>L11905.1</u>	<u>CGYMTCYTB</u>	Cratogeomys gymnurus mitochondrial c...	44	0.001
<u>gb</u>	<u>U34679.1</u>	<u>P0U34679</u>	Philander opossum cytochrome b light s...	44	0.001
<u>gb</u>	<u>L11907.1</u>	<u>CGYMTCYTB3F</u>	Cratogeomys goldmani rubellus mitoch...	44	0.001
<u>gb</u>	<u>L11906.1</u>	<u>CGYMTCYTB3E</u>	Cratogeomys merriami mitochondrial c...	44	0.001
<u>gb</u>	<u>L11902.1</u>	<u>CGYMTCYTB3A</u>	Cratogeomys castanops castanops mito...	44	0.001
<u>emb</u>	<u>X92524.1</u>	<u>SLCYTB</u>	S.longirostris cytochrome b gene (compl...	44	0.001
<u>gb</u>	<u>U46771.1</u>	<u>ACU46771</u>	Anthus campestris cytochrome b gene, m...	44	0.001
<u>dbi</u>	<u>AB021773.1</u>	<u>AB021773</u>	Anguilla interioris mitochondrial c...	44	0.001
<u>dbi</u>	<u>AB006953.1</u>	<u>AB006953</u>	Carassius auratus langsdorfi mitoch...	44	0.001
<u>emb</u>	<u>Z73492.1</u>	<u>MTPTRCYTB</u>	P.trochilus mitochondrial cytochrome...	44	0.001
<u>dbi</u>	<u>AB035239.1</u>	<u>AB035239</u>	Osteoglossum ferreirai mitochondria...	44	0.001
<u>emb</u>	<u>X92532.1</u>	<u>MMCYTB2</u>	M.monoceros cytochrome b gene (complet...	44	0.001
<u>emb</u>	<u>X74260.1</u>	<u>MIVOCYTE</u>	V.olivaceus mitochondrion gene for cy...	44	0.001
<u>emb</u>	<u>X56293.1</u>	<u>MISLCYTB3B</u>	S.longirostris mitochondrion cytb gen...	44	0.001
<u>emb</u>	<u>X56292.1</u>	<u>MISLCYTB3A</u>	S.longirostris mitochondrion cytb ge...	44	0.001
<u>emb</u>	<u>X74256.1</u>	<u>MIPVCYTB3</u>	P.violaceus mitochondrion gene for cy...	44	0.001
<u>emb</u>	<u>X82304.1</u>	<u>MIPFCYTB3G</u>	P.hispida mitochondrial cytochrome b...	44	0.001
<u>emb</u>	<u>X82302.1</u>	<u>MIPFCYTB3G</u>	P.fasciata mitochondrial cytochrome ...	44	0.001
<u>emb</u>	<u>X56284.1</u>	<u>MIOACYTB3</u>	O.aries mitochondrion cytb gene for c...	44	0.001
<u>emb</u>	<u>X74252.1</u>	<u>MIMKCYTB3</u>	M.keraudrenii mitochondrion gene for ...	44	0.001
<u>emb</u>	<u>X72005.1</u>	<u>MILWCYTB3</u>	L.weddelli mitochondrial gene for cyt...	44	0.001
<u>emb</u>	<u>X74259.1</u>	<u>MILLCYTB3</u>	L.ludovicianus mitochondrion gene for...	44	0.001
<u>emb</u>	<u>Y08814.1</u>	<u>MILHLCYTB3G</u>	H.liberiensis mitochondrial cytochro...	44	0.001
<u>emb</u>	<u>Y08813.1</u>	<u>MIHACYTB3</u>	H.amphibius mitochondrial cytochrome ...	44	0.001
<u>emb</u>	<u>X56287.1</u>	<u>MIGCCYTB3</u>	G.camelopardalis mitochondrion cytb g...	44	0.001
<u>emb</u>	<u>X74253.1</u>	<u>MIEFCYTB3</u>	E.fastuosus mitochondrion gene for cy...	44	0.001
<u>emb</u>	<u>X60941.1</u>	<u>MIEACB333</u>	Epimachus albertisii mitochondrial ge...	44	0.001
<u>emb</u>	<u>X74255.1</u>	<u>MIDMCYTB3</u>	D.magnificus mitochondrion gene for c...	44	0.001
<u>emb</u>	<u>X56289.1</u>	<u>MICHCYTB3</u>	C.hircus mitochondrion cytb gene for ...	44	0.001
<u>emb</u>	<u>V00654.1</u>	<u>MIBTICKX</u>	Bos taurus complete mitochondrial genome	44	0.001
<u>emb</u>	<u>X50940.1</u>	<u>MIAMCB333</u>	A.macgregoriae mitochondrial gene for...	44	0.001
<u>emb</u>	<u>X92530.1</u>	<u>LACYTB3</u>	L.albirostris cytochrome b gene (comple...	44	0.001
<u>gb</u>	<u>U09265.1</u>	<u>CAU09265</u>	Coccycuas americanus mitochondrion cyto...	44	0.001
<u>dbi</u>	<u>AB023905.1</u>	<u>AB023905</u>	Petaurista leucogenys mitochondrial...	44	0.001
<u>dbi</u>	<u>AB023905.1</u>	<u>AB023905</u>	Petaurista leucogenys mitochondrial...	44	0.001
<u>dbi</u>	<u>AB023904.1</u>	<u>AB023904</u>	Petaurista leucogenys mitochondrial...	44	0.001
<u>dbi</u>	<u>AB023903.1</u>	<u>AB023903</u>	Petaurista leucogenys mitochondrion...	44	0.001
<u>dbi</u>	<u>D88983.1</u>	<u>D88983</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbi</u>	<u>D88638.1</u>	<u>D88638</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbi</u>	<u>D88636.1</u>	<u>D88636</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbi</u>	<u>D88635.1</u>	<u>D88635</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbi</u>	<u>D88633.1</u>	<u>D88633</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbi</u>	<u>D88632.1</u>	<u>D88632</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbi</u>	<u>D88630.1</u>	<u>D88630</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbi</u>	<u>D88628.1</u>	<u>D88628</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbi</u>	<u>D88627.1</u>	<u>D88627</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbi</u>	<u>D84204.1</u>	<u>GOTMTCB3D</u>	Capra aegagrus mitochondrial DNA for ...	44	0.001
<u>dbi</u>	<u>D84202.1</u>	<u>GOTMTCB8B</u>	Capra falconeri mitochondrial DNA for ...	44	0.001
<u>dbi</u>	<u>D82891.1</u>	<u>D82891</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbi</u>	<u>D82892.1</u>	<u>D82892</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbi</u>	<u>D82889.1</u>	<u>D82889</u>	Bos javanicus mitochondrial DNA for cyc...	44	0.001
<u>dbi</u>	<u>D12121.1</u>	<u>BBUMTCB21</u>	Bubalus arnee bubalis mitochondrial ...	44	0.001
<u>dbi</u>	<u>D14521.1</u>	<u>BBUMTCB8A</u>	Bubalus bubalis mitochondrial gene co...	44	0.001
<u>dbi</u>	<u>A8004074.1</u>	<u>A8004074</u>	Capra hircus mitochondrial DNA coc ...	44	0.001
<u>dbi</u>	<u>A8004072.1</u>	<u>A8004072</u>	Capra hircus mitochondrial DNA coc ...	44	0.001
<u>dbi</u>	<u>A8004071.1</u>	<u>A8004071</u>	Capra hircus mitochondrial DNA coc ...	44	0.001
<u>dbi</u>	<u>A8004052.1</u>	<u>A8004052</u>	Capra aegagrus mitochondrial DNA co...	44	0.001
<u>dbi</u>	<u>D99540.1</u>	<u>D99540</u>	Anoa depressicornis mitochondrial DNA c...	44	0.001
<u>dbi</u>	<u>D99517.1</u>	<u>D99517</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001

<u>dbj D88634.1 D88634</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbj D88631.1 D88631</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbj D88629.1 D88629</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbj D84205.1 SHPMCBE</u>	Sheep mitochondrial DNA for cytochrom...	44	0.001
<u>dbj D84203.1 SHPMCBC</u>	Ovis musimon mitochondrial DNA for cy...	44	0.001
<u>dbj D84201.1 GOTMCBA</u>	Goat mitochondrial DNA for cytochrome...	44	0.001
<u>dbj D82894.1 D82894</u>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<u>dbj D82891.1 D82891</u>	Bubalus quarlesi mitochondrial DNA for ...	44	0.001
<u>dbj D34638.1 BBUMTCBB</u>	Bubalus bubalis mitochondrial gene fo...	44	0.001
<u>dbj D34636.1 BOVMTCBB</u>	Bos javanicus mitochondrial gene for ...	44	0.001
<u>dbj AB037602.1 AB037602</u>	Talpa altaica mitochondrial cytb ge...	44	0.001
<u>dbj AB018985.1 AB018985</u>	Cichlasoma citrinellum mitochondria...	44	0.001
<u>dbj AB004075.1 AB004075</u>	Capra hircus mitochondrial DNA for ...	44	0.001
<u>dbj AB004073.1 AB004073</u>	Capra hircus mitochondrial DNA for ...	44	0.001
<u>dbj AB004070.1 AB004070</u>	Capra hircus mitochondrial DNA for ...	44	0.001
<u>emb X92531.1 DLCYTB</u>	D.leucas cytochrome b gene (complete se...	44	0.001
<u>gb U07565.1 HAU07565</u>	Hippopotamus amphibius mitochondrion c...	44	0.001
<u>gb U10367.1 PVU10367</u>	Ptilonorhynchus violaceus mitochondrio...	44	0.001
<u>gb U10364.1 CMU10364</u>	Chlamydera maculata mitochondrion cyto...	44	0.001
<u>emb Z96068.1 ASZ96068</u>	Acomys spinosissimus DNA for mitochon...	42	0.005
<u>gb U76507.1 AIU76507</u>	Amblyornis inornatus cytochrome b gene...	40	0.021
<u>gb AF157466.1 AF157466</u>	Lepus timidus cytochrome b (Cyb) gen...	40	0.021
<u>gb AF157464.1 AF157464</u>	Lepus corsicanus haplotype 1 cytochr...	40	0.021
<u>gb AF157463.1 AF157463</u>	Lepus corsicanus haplotype 3 cytochr...	40	0.021
<u>gb AY016019.1 AY016018S3</u>	Mullerornis agilis cytochrome b ge...	40	0.021
<u>gb AF027330.1 </u>	Akodon olivaceus canescens museum catalog nu...	40	0.021
<u>gb AF027329.1 </u>	Akodon olivaceus canescens museum catalog nu...	40	0.021
<u>gb AF027328.1 </u>	Akodon olivaceus canescens museum catalog nu...	40	0.021
<u>gb AF027327.1 </u>	Akodon olivaceus canescens museum catalog nu...	40	0.021
<u>gb AF027326.1 </u>	Akodon olivaceus canescens museum catalog nu...	40	0.021
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<u>gb AF027322.1 </u>	Akodon olivaceus beatus museum catalog numbe...	40	0.021
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<u>gb AF027310.1 </u>	Akodon olivaceus brachiotis museum catalog n...	40	0.021
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<u>gb AF266188.1 AF266188</u>	Gillichthys mirabilis cytochrome b m...	40	0.021
<u>gb AF324034.1 AF324034</u>	Phyllobates aurotaenia isolate Quebr...	40	0.021
<u>gb AF272639.1 AF272639</u>	Clethrionomys gapperi specimen-vouch...	40	0.021
<u>gb AF272636.1 AF272636</u>	Clethrionomys gapperi specimen-vouch...	40	0.021
<u>gb AF272634.1 AF272634</u>	Clethrionomys gapperi specimen-vouch...	40	0.021
<u>gb AF272633.1 AF272633</u>	Clethrionomys gapperi specimen-vouch...	40	0.021
<u>gb AF182711.1 AF182711</u>	Geopelia cuneata cytochrome b gene.	40	0.021
<u>gb AF182687.1 AF182687</u>	Columbina picui cytochrome b gene. p...	40	0.021
<u>gb AF155422.1 AF155422</u>	Sigmmodon ochrognathus cytochrome b (...	40	0.021
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<u>gb AF155395.1 AF155395</u>	Peromyscus attwateri isolate lb cyto...	40	0.021
<u>gb AF155394.1 AF155394</u>	Peromyscus attwateri isolate la cyto...	40	0.021
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<u>gb AF155590.1 AF155590</u>	Sigmmodon ochrognathus isolate Duran4...	40	0.021
<u>gb AF155589.1 AF155589</u>	Sigmmodon ochrognathus isolate ElEnt8...	40	0.021
<u>gb AF155588.1 AF155588</u>	Sigmmodon ochrognathus isolate Bb-end4...	40	0.021
<u>gb AF122521.1 AF122521</u>	Trachypönus dalmudii cytochrome b ...	40	0.021
<u>gb AF125147.1 AF125147</u>	Ureus apodus cytochrome b gene. co...	40	0.021
<u>gb AF120531.1 AF120531</u>	Podarcis sicula cytochrome b gene. P...	40	0.021
<u>gb AF121705.1 AF121705</u>	Hippocampus zosterae haplotype FK.14...	40	0.021
<u>gb MC000991.1 Carvus porcellus</u>	porcellus complex mitochondrial genome	40	0.021

<u>gb AF004572.1 AF004572</u>	Arvicanthis niloticus cytochrome b (...	<u>40</u>	<u>0.021</u>
<u>gb AF088932.1 AF088932</u>	Sminthopsis psammophila cytochrome b...	<u>40</u>	<u>0.021</u>
<u>gb U62697.1 ORUCYTB2</u>	Oreopholus ruficollis cytochrome b (cy...	<u>40</u>	<u>0.021</u>
<u>gb U62681.1 CACYTB2</u>	Charadrius australis cytochrome b (cyt ...	<u>40</u>	<u>0.021</u>
<u>gb U62707.1 CVERCYTB2</u>	Charadrius veredus cytochrome b (cytb...)	<u>38</u>	<u>0.084</u>
<u>emb AJ004315.1 HCAJ4315</u>	Hippolais caligata mitochondrial cy...	<u>38</u>	<u>0.084</u>

Alignments

<u>tmpseq_0</u>	1	cctccctagttgttagggattgatcg	26
<u>AF189111</u>	797	772
<u>U86834</u>	858	833
<u>AF123633</u>	56	31
<u>AF123617</u>	104	79
<u>AF127202</u>	107	82
<u>AF127194</u>	107	82
<u>AF217828</u>	845	820
<u>AF160578</u>	869	844
<u>AF009931</u>	869	844
<u>AF091629</u>	869	844
<u>AF034967</u>	869	844
<u>AF038290</u>	869	844
<u>U07577</u>	869	844
<u>U81343</u>	.791	766
<u>AJ222681</u>	869	844
<u>M99464</u>	869	844
<u>AJ225116</u>	869	844
<u>U25738</u>	872	847
<u>U25736</u>	872	847
<u>U15202</u>	872	847
<u>U15204</u>	872	844
<u>X56290</u>	869	844
<u>X56286</u>	869	844
<u>D88639</u>	869	844
<u>D82890</u>	869	844
<u>AF119261</u>	869	847
<u>AF123615</u>	101	79
<u>AF150603</u>	866	844
<u>U62687</u>	179	157
<u>U62685</u>	179	157
<u>AF022071</u>	866	844
<u>AF022070</u>	866	844
<u>U83317</u>	872	850
<u>U37293</u>	774	752
<u>U37292</u>	774	752
<u>U37291</u>	774	752
<u>AF082055</u>	51	29
<u>U72770</u>	798	776
<u>U07578</u>	869	847
<u>AF011908</u>	187	165
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<u>AJ004230</u>	773	751
<u>AJ004229</u>	773	751
<u>AJ004232</u>	773	751
<u>U88865</u>	850	828
<u>U90001</u>	536	514
<u>U61057</u>	773	751
<u>AB016404</u>	173	151
<u>AB016402</u>	173	151
<u>AB016400</u>	173	151
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<u>U19511</u>	774	752
<u>X92519</u>	869	847
<u>L08011</u>	872	850
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<u>AF971591</u>	677	652
<u>AX005212</u>	761	736
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<u>AF081962</u>	754c.....	729
<u>AF081961</u>	872c.....	847
<u>AF081960</u>	872g.....	847
<u>AF081959</u>	872c.....	847
<u>AF112405</u>	869c.....	844
<u>AF144317</u>	161g.....	136
<u>AF144316</u>	161g.....	136
<u>AF144315</u>	161g.....	136
<u>AF144314</u>	161g.....	136
<u>AF144313</u>	161g.....	136
<u>AF144312</u>	161g.....	136
<u>AF144311</u>	161g.....	136
<u>AF144310</u>	161g.....	136
<u>AF144309</u>	161g.....	136
<u>NC_001567</u>	15382g.....	15357
<u>AF212124</u>	425c.....	400
<u>AF182706</u>	739a.....	714
<u>AF010406</u>	15027a.....	15002
<u>AF096452</u>	735c.....	710
<u>AF283619</u>	845a.....	820
<u>AF283618</u>	845a.....	820
<u>AF283608</u>	845a.....	820
<u>AF283602</u>	845a.....	820
<u>AF310059</u>	770a.....	745
<u>AF145616</u>	95g.....	70
<u>AF271410</u>	869g.....	844
<u>AF290112</u>	752g.....	727
<u>NC_002504</u>	15022g.....	14997
<u>AF163901</u>	869g.....	844
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<u>AF188454</u>	91a.....	66
<u>AF163925</u>	869c.....	844
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<u>AF121517</u>	68g.....	43
<u>AF121516</u>	104g.....	77
<u>AF121515</u>	68g.....	43
<u>AF121511</u>	64g.....	57

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<u>AF123628</u>	104g.....	79
<u>AF123621</u>	85g.....	60
<u>AF123619</u>	104g.....	79
<u>AF123618</u>	104g.....	79
<u>AF123614</u>	104g.....	79
<u>AF123613</u>	101g.....	76
<u>AF127201</u>	107g.....	82
<u>AF127192</u>	107c.....	82
<u>AF127189</u>	107g.....	82
<u>AF197849</u>	872g.....	847
<u>AF197847</u>	872c.....	847
<u>NC 000889</u>	15040g.....	15015
<u>NC 002079</u>	16164g.....	16139
<u>NC 001794</u>	15052a.....	15027
<u>NC 001610</u>	15045c.....	15020
<u>AF201612</u>	520c.....	495
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<u>AF097927</u>	869g.....	844
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<u>AF168760</u>	507a.....	482
<u>AF168759</u>	507a.....	482
<u>AF168758</u>	507a.....	482
<u>AF168756</u>	507a.....	482
<u>AF182381</u>	692c.....	667
<u>AF182380</u>	692c.....	667
<u>U89187</u>	872a.....	847
<u>AF193833</u>	773g.....	748
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<u>AF193821</u>	773a.....	748
<u>AF217837</u>	845c.....	820
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<u>AF217815</u>	845c.....	820
<u>AF118156</u>	101g.....	76
<u>AF209938</u>	418a.....	393
<u>AF209933</u>	418a.....	393
<u>AF059104</u>	776c.....	751
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<u>AF160612</u>	869g.....	844
<u>AF160611</u>	238g.....	213
<u>AF160610</u>	869g.....	844
<u>AF160604</u>	869g.....	844
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<u>AF016287</u>	869g.....	844
<u>AF016286</u>	869g.....	844
<u>AF016281</u>	869a.....	844
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<u>AF108673</u>	869	g.....	844
<u>AF108669</u>	857	g.....	832
<u>AF042720</u>	869	a.....	844
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<u>AF157915</u>	869	a.....	844
<u>AF157914</u>	869	a.....	844
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<u>AF157891</u>	869	g.....	844
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<u>AF030497</u>	50	a.....	25
<u>U03541</u>	869	g.....	844
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<u>AF009941</u>	869	g.....	844
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<u>AF094618</u>	737	t.....	712
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<u>AF022057</u>	869	g.....	844
<u>AF022054</u>	869	a.....	844
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<u>U69844</u>	845	t.....	820
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<u>AF121222</u>	140	g.....	115
<u>AF096625</u>	869	g.....	844
<u>AF096624</u>	869	g.....	844
<u>AF081052</u>	869	a.....	844
<u>AF081049</u>	869	a.....	844
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<u>AF082063</u>	54	g.....	29
<u>AJ010957</u>	15040	g.....	15015
<u>U76506</u>	773	g.....	748
<u>U76504</u>	773	g.....	748
<u>U76505</u>	773	c.....	748
<u>U76503</u>	773	t.....	748
<u>U76508</u>	773	t.....	748
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<u>AF051876</u>	869	t.....	844
<u>AF082007</u>	872	t.....	847
<u>AF082006</u>	872	t.....	847
<u>AF082005</u>	872	t.....	847
<u>AF082004</u>	872	t.....	847
<u>AF082002</u>	872	t.....	847
<u>AF082001</u>	872	t.....	847
<u>AF082000</u>	872	t.....	847
<u>AF081999</u>	872	t.....	847

<u>AF081998</u>	872t.....	847
<u>AF081997</u>	872t.....	847
<u>AF081996</u>	872t.....	847
<u>AF081995</u>	872t.....	847
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<u>US3580</u>	869g.....	844
<u>US3577</u>	869g.....	844
<u>US3576</u>	869a..t..	844
<u>Y95512</u>	31g.....	6
<u>Y95508</u>	31a.....	6
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<u>U17867</u>	869g.....	844
<u>U17860</u>	869g.....	844
<u>U17859</u>	800g.....	775
<u>AJ010556</u>	869g.....	844
<u>AF034736</u>	869g.....	844
<u>AF034730</u>	869a.....	844
<u>AF034729</u>	869a.....	844
<u>AF034728</u>	869g.....	844
<u>AF034727</u>	869a.....	844
<u>AF034724</u>	869g.....	844
<u>AF034722</u>	869g.....	844
<u>U72038</u>	869g.....	844
<u>U72037</u>	869g.....	844
<u>M99455</u>	869a.....	844
<u>L29055</u>	260a.....	235
<u>AF082047</u>	54g.....	29
<u>AF038286</u>	869t.....	844
<u>AF038284</u>	869t.....	844
<u>AF059093</u>	776t.....	751
<u>AF059092</u>	776t.....	751
<u>AF059091</u>	776t.....	751
<u>AF059080</u>	776t..t..	751
<u>AF059078</u>	776t..t..	751
<u>AF052240</u>	61a.....	36
<u>AF006240</u>	774t.....	749
<u>AF006227</u>	774g.....	749
<u>AF047447</u>	41g.....	16
<u>U07576</u>	869g.....	844
<u>AF028180</u>	65g.....	40
<u>AF028178</u>	69g.....	44
<u>AF028170</u>	77g.....	52
<u>M99454</u>	869a.....	844
<u>M99451</u>	869t.....	844
<u>U23461</u>	869c.....	844
<u>Y87138</u>	869g.....	844
<u>U07590</u>	869g.....	844
<u>AJ004126</u>	773c.....	748
<u>AF020255</u>	819g.....	794
<u>Y19184</u>	15022g.....	14997
<u>U88862</u>	843a.....	818
<u>U88859</u>	867g.....	842
<u>U88858</u>	843c.....	818
<u>U88857</u>	863g.....	838
<u>U88856</u>	867g.....	842
<u>Y10534</u>	15052a.....	15027
<u>U81157</u>	791t.....	766
<u>U81156</u>	791a.....	766
<u>U73154</u>	452a.....	427
<u>U77113</u>	872g.....	847
<u>Z29371</u>	15045t.....	15020
<u>AJ2223679</u>	869g.....	844
<u>AJ2223680</u>	869a.....	844
<u>AJ2223681</u>	869g.....	844
<u>M22168</u>	869a.....	844
<u>G22132</u>	869c.....	844

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<u>AF272611</u>	869		850
<u>AF182711</u>	712		691
<u>AF193697</u>	774		755
<u>AF153422</u>	669		850
<u>AF153402</u>	669		850
<u>AF153395</u>	669		850
<u>AF153381</u>	669		850
<u>AF153392</u>	669		850
<u>AF153321</u>	669		850
<u>AF153322</u>	669		850

<u>AF155589</u>	869	850
<u>AF155588</u>	869	850
<u>AF121531</u>	771	752
<u>AF264047</u>	869	850
<u>AF206531</u>	771	752
<u>AF192706</u>	863	844
<u>NC_000884</u>	15032	15013
<u>AF004572</u>	869	850
<u>AF088932</u>	869	850
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<u>U62681</u>	179	160
<u>U62707</u>	179g.....n..	154
<u>AJ004315</u>	773t.....n....	748

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885

Number of sequences in database: 807,597

Lambda K H
1.37 0.711 1.31

Gapped

Lambda K H
1.37 0.711 1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 19068

Number of Sequences: 807597

Number of extensions: 19068

Number of successful extensions: 7580

Number of sequences better than 10.0: 2441

length of query: 26

length of database: 2,863,827,885

effective HSP length: 17

effective length of query: 9

effective length of database: 2,850,098,736

effective search space: 25650888624

effective search space used: 25650888624

T: 0

A: 30

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 16 (32.1 bits)

Table 12. The other animals belonging to distantly related species analyzed by our primers to demonstrate its universal nature

SN.	Name of the animal
1.	Indian black buck no.1
2.	Indian black buck no 2
3	sheep
4	pig
5	dog
6	chimpanzee (chimss)
7	human (humsk)
8	Hamster
9	crocodile no1
10	crocodile no2
11	turtle no1
12	turtle no2
13	mouse
14	varanus
15	Naga-naga snake
16	Indian elephant
17	hen
18	dugong
19	lizard
20	weaver bird no 1
21	weaver bird no.2
22	buffalo no 1
23	buffalo no 2

CLAIMS

1 Universal primers named as 'mcb 398' and 'mcb 869' capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level, said primers, having the sequences:

primers name	Sequence (5'-3')
mcb 398	"TACCATGAGGACAAATATCATTCTG"
mcb 869	"CCTCCTAGTTGTTAGGGATTGATCG"

5 2. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is capable of significantly discriminating amongst various evolutionary lineages 10 of different animal species.

2. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is flanked by the highly conserved sequences amongst a vast range of animal species.

15 3. Primers as claimed in claim 1 wherein the fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.

4. Primers as claimed in claim 1 wherein in *Antilope cervicapra* species, the sequences of 15 the fragment mentioned under claim 1 are as follows:

20 Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*:
"taccatgaggacaaatatcttttgaggagcaacagtcatcaccaatctccttcagcaatccatacatcggtacaaacctag
tagaatgaatctgaggagggttcgttagataaagcaacccttacccgattttcgcccttcactttatcctccatttatcattgc
agcccttaccatagtacacctactgtttccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaa
attccatccacccctactacactatcaaagatatccttaggagctctactatataatttaaccctcatgctctagtccatttcacc
ggacctgtttggagacccagacaactatacaccagcaaacccttaatacacccccacatatcaagcccgaatgatacttc
ctatttgcatacgcaatccctcgatcaattcctaacaacttaggagg"

25 6. A method for the identification of the animal from a biological sample, said method comprising the steps of:

- isolating and amplifying the DNA from the biological sample to be tested using the primers as claimed in claim 1,
- sequencing the amplified products,
- blasting the sequence resolved in step (b) against mito database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely family of the animal source of the biological sample.

d) blasting the sequence resolved in step (b) against non-redundant (nr) database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely genus, species or more precisely the sub-species of the animal source of the biological sample,

5 e) identifying the most significant alignment of the sequence resolved with cytochrome b gene sequence of the animal identified in steps (c) and (d) respectively and selection of these animals as 'reference animals' for further studies,

10 f) isolating and amplifying and sequencing the DNA sequences from the reference animal on both strands in triplicate using the primers as claimed in claim 1,

g) aligning the sequences obtained using CLUSTRAL program and identifying the variable sites amongst the animals analyzed,

15 h) comparing the nucleotide sequences pair-wise to determine the variation among the animals resolved and identifying the nucleotide sequence to which the DNA sequence of the biological sample bears maximum similarity as the source animal of the biological sample.

7. A method as claimed in claim 6 wherein the universal PCR protocol works universally with the DNA template of any unknown animal origin and the universal primers mentioned under column 4.

20 8. A method as claimed in claim 6 wherein the Amplification reactions should be carried out in 20 µl reaction volume containing approximately 20 ng of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles should be held for 10 min.

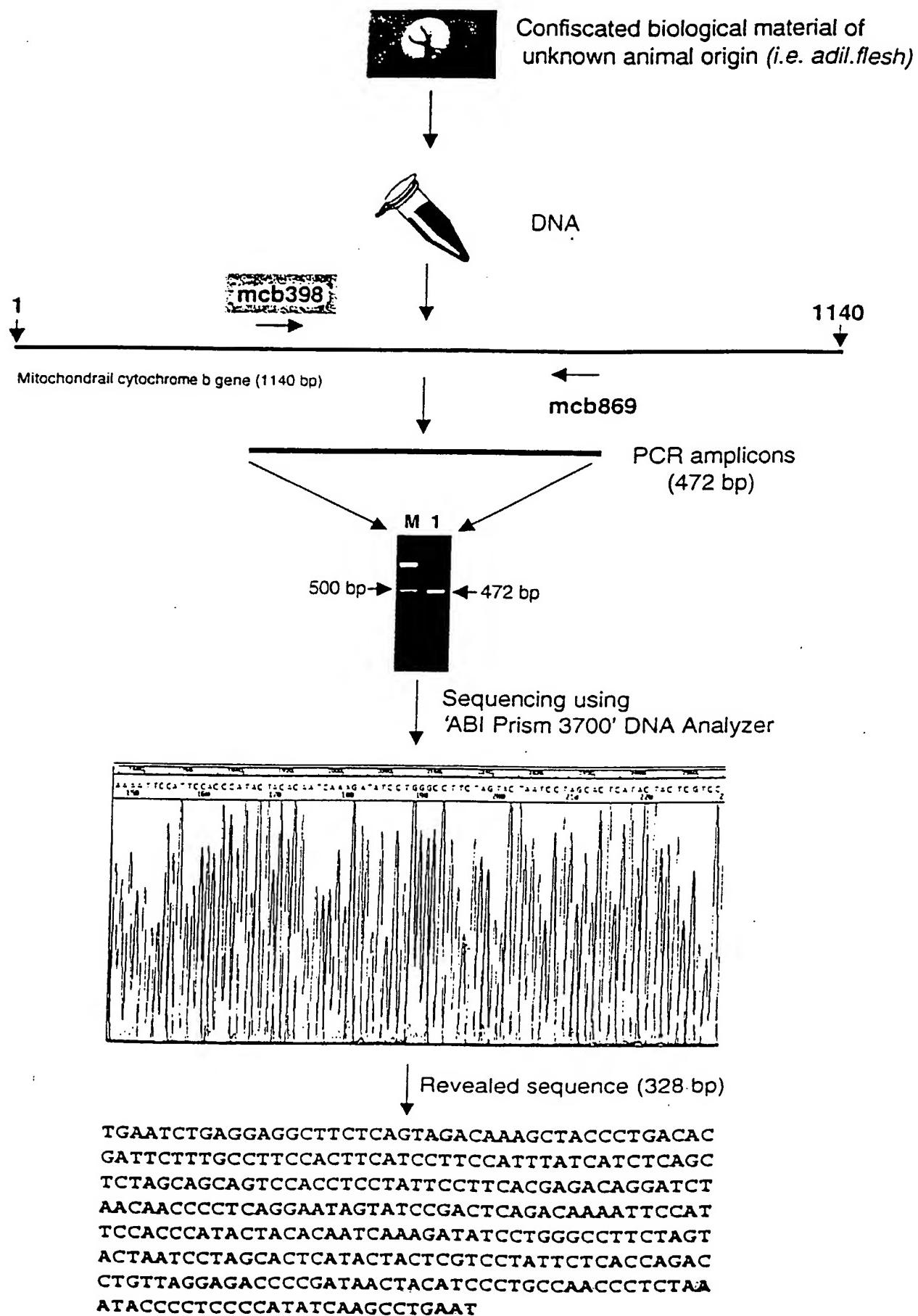
25 9. A method as claimed in claim 6 wherein the method enables identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

30 10. A method as claimed in claim 6 wherein the method is used for animal identification to establish the crime with the criminal beyond a reasonably doubt.

11. A method as claimed in claim 6 wherein the method is used to establish the identity of

biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

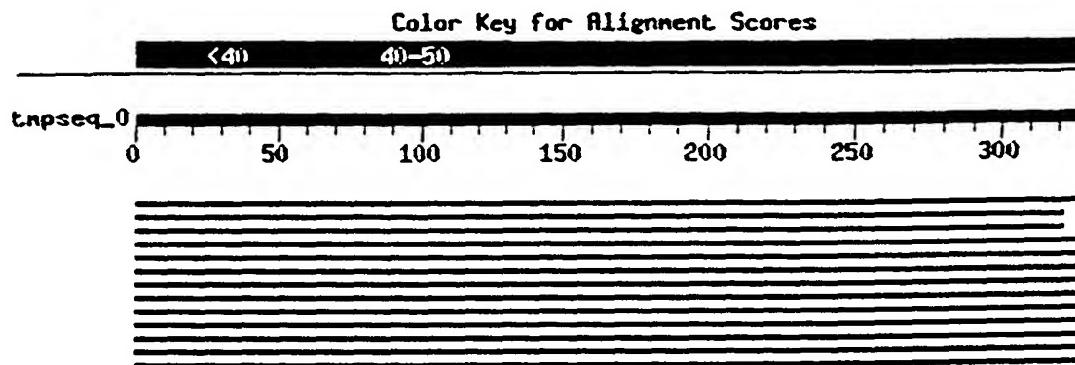
12. A method as claimed in claim 6 wherein the method is used for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation of the wildlife resources could be controlled.
- 5 13. A method as claimed in claim 6 wherein the method is used to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented.
- 10 14. A method as claimed in claim 6 wherein the method is used for animal identification to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies.
- 15 15. A method as claimed in claim 6 wherein the method is used to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.
16. A method as claimed in claim 6 wherein the method is used so that it can be converted to a (a) COMMERCIAL 'MOLECUALR KIT' and (b) 'DNA CHIPS' based applications for wildlife identification in forensics.
- 20

**Figure 1 a**

Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. 'adil.flesh' using primers 'mcb398' and 'mcb869'

Homology search in 'nr' database using 'BLAST'

<http://www.ncbi.nlm.nih.gov/BLAST/>



Sequences producing significant alignments:	Score (bits)	E Value
gb AY005809.1 <i>Panthera pardus</i> cytochrome b gene, partial c...	603	e-170
gb AF053054.1 AF053054 <i>Panthera tigris sumatrae</i> isolate Su1...	527	e-147
gb AF053053.1 AF053053 <i>Panthera tigris tigris</i> isolate B7 mi...	527	e-147
gb AF053050.1 AF053050 <i>Panthera tigris corbetti</i> isolate C2 ...	476	e-132
gb AF053049.1 AF053049 <i>Panthera tigris corbetti</i> isolate C1 ...	476	e-132

Selection of reference animals based on above information and further analysis using primers 'mcb398' and 'mcb869'

Multiple sequence alignments using 'Autoassembler'

Sequence alignment showing multiple reference sequences aligned against the target sequence. The alignment highlights conserved regions and differences between species.

Figure 1 b

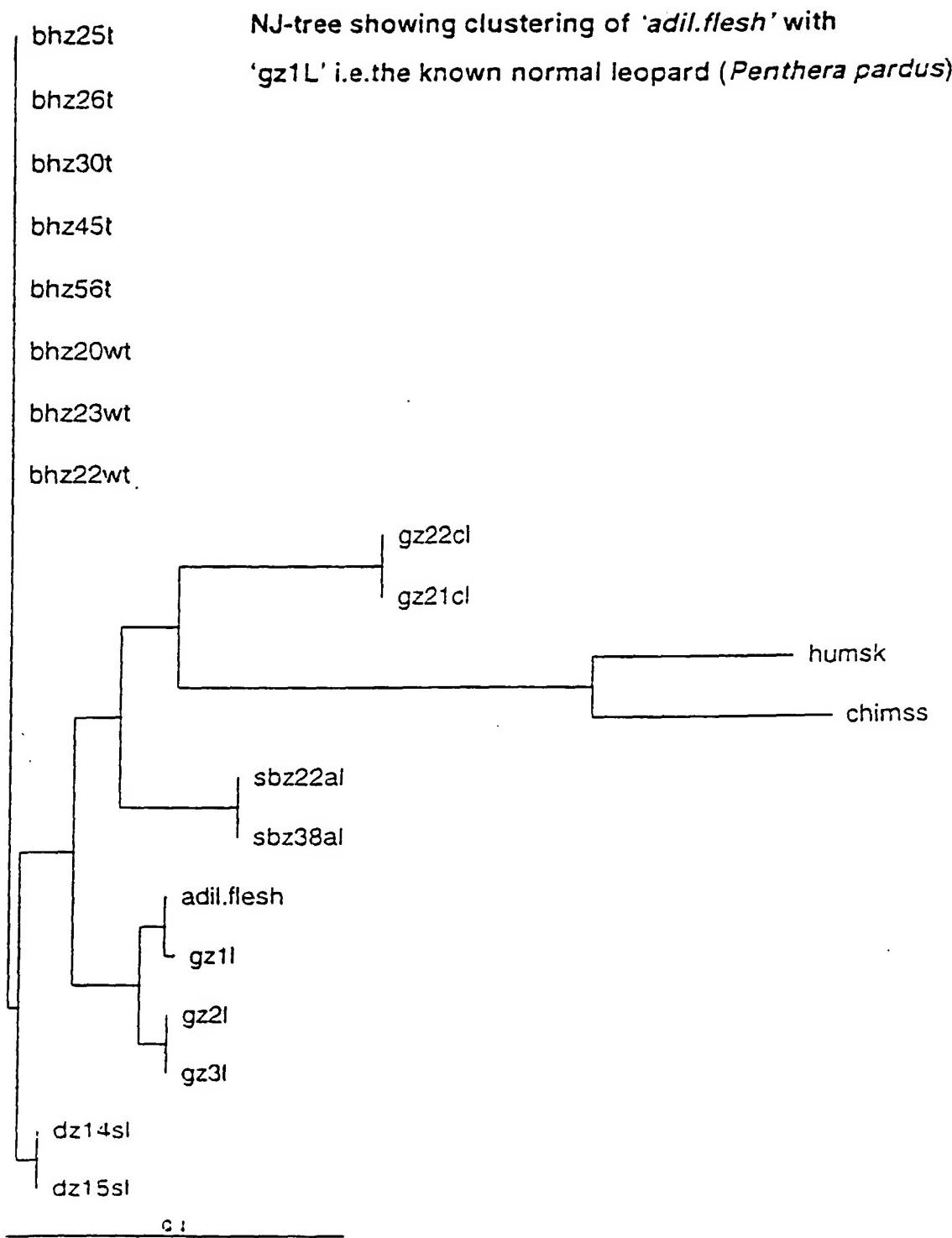


Figure 1c

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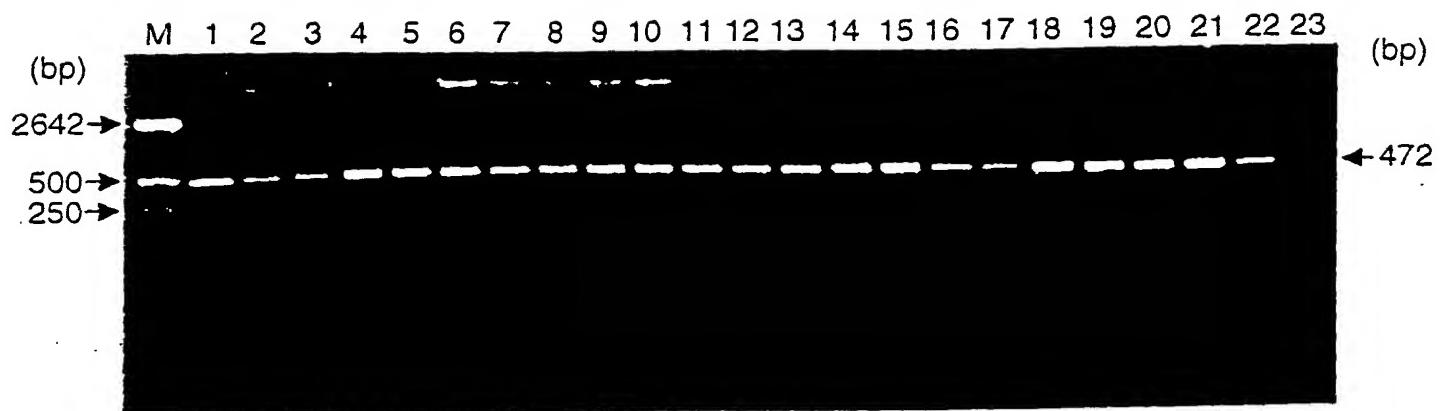


Figure 2

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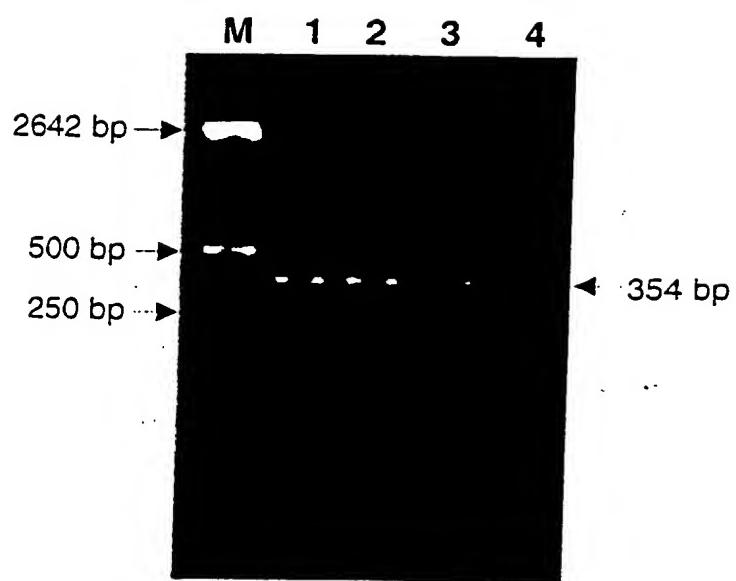


Figure 3

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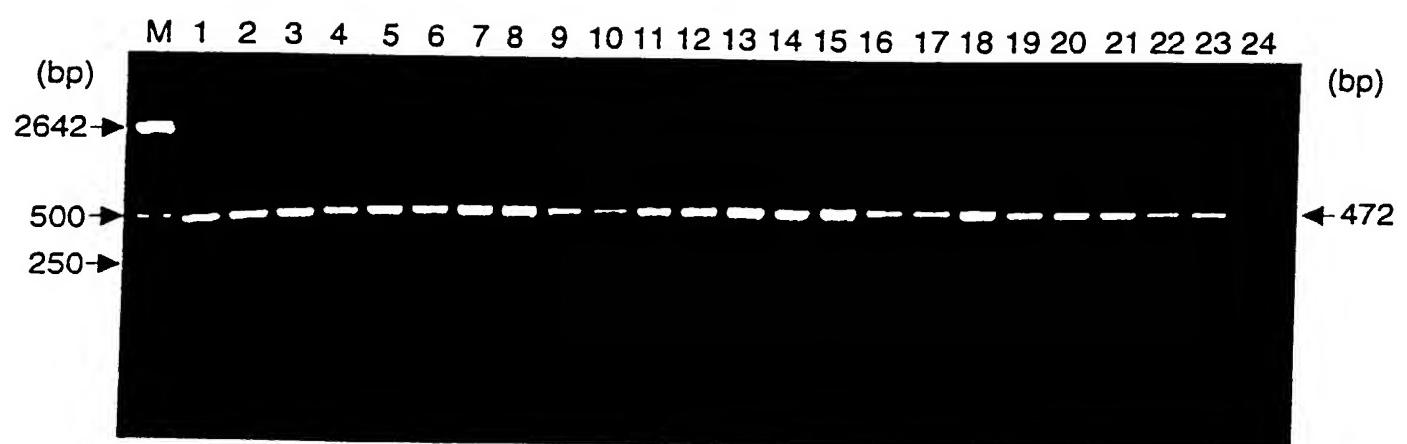


Figure 4

INTERNATIONAL SEARCH REPORT

Inte	Application No
PCT/IN 01/00055	

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
--

BIOSIS, EPO-Internal, EMBL, WPI Data, PAJ, MEDLINE, EMBASE
--

C. DOCUMENTS CONSIDERED TO BE RELEVANT
--

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KOCHER T D ET AL: "DYNAMICS OF MITOCHONDRIAL DNA EVOLUTION IN ANIMALS AMPLIFICATION AND SEQUENCING WITH CONSERVED PRIMERS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 86, no. 16, 1989, pages 6196-6200, XP002189444 1989 ISSN: 0027-8424 the whole document ---	1-16
Y	WO 92 05277 A (DAVIDSON WILLIAM SCOTT ; BARTLETT SYLVIA ERNESTINE (CA)) 2 April 1992 (1992-04-02) the whole document ---	1-16 -/-

<input checked="" type="checkbox"/> Further documents are listed in the continuation of box C.
--

<input checked="" type="checkbox"/> Patent family members are listed in annex.
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° Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *&* document member of the same patent family

Date of the actual completion of the international search

28 February 2002

Date of mailing of the international search report
--

12/03/2002

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016

Authorized officer

Hagenmaier, S

INTERNATIONAL SEARCH REPORT

Inte	Application No
PCT/IN 01/00055	

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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Y	DATABASE EMBL 'Online!' ID/AC AAF56513, 28 November 2000 (2000-11-28) ZH NIPPON KAGAKU SENI KENSA KYOKAI: "Animal fibre identification PCR primer #3" XP002191314 abstract ---	1-16
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Y	EP 0 807 690 A (KARL SCHMITZ SCHOLL FONDS FUER) 19 November 1997 (1997-11-19) the whole document ---	1-16
Y	MATTHEE CONRAD A ET AL: "Cytochrome b phylogeny of the family Bovidae: Resolution within the Alcelaphini, Antilopini, Neotragini, and Tragelaphini." MOLECULAR PHYLOGENETICS AND EVOLUTION, vol. 12, no. 1, June 1999 (1999-06), pages 31-46, XP001053239 ISSN: 1055-7903 the whole document ---	1-16
Y	SHANKARANARAYANAN PATTABHIRAMAN ET AL: "Mitochondrial DNA sequence divergence among big cats and their hybrids." CURRENT SCIENCE (BANGALORE), vol. 75, no. 9, 10 November 1998 (1998-11-10), pages 919-923, XP001063942 ISSN: 0011-3891 the whole document ---	1-16
A	THOMPSON JULIE D ET AL: "A comprehensive comparison of multiple sequence alignment programs." NUCLEIC ACIDS RESEARCH, vol. 27, no. 13, 1 July 1999 (1999-07-01), pages 2682-2690, XP002191669 ISSN: 0305-1048 the whole document -----	

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Information on patent family members

Int	Application No
PCT/EP	01/00055

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			EP	0550491 A1		14-07-1993
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			WO	9315215 A1		05-08-1993
			US	5565320 A		15-10-1996
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			EP	0807690 A1		19-11-1997
			WO	9743618 A2		20-11-1997